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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:34:32 ; Search time 12 Seconds  
(without alignments)  
79.718 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPBEQYWAALLGTCMFC.....FPQLPPTQLSGLSPNIGGLL 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 199.5 | 24.8        | 292    | 6     | US-10-967-527A-19  |
| 2          | 195   | 24.3        | 293    | 6     | US-10-742-634-7    |
| 3          | 180   | 22.4        | 293    | 6     | US-10-967-527A-20  |
| 4          | 107.5 | 13.4        | 249    | 6     | US-10-967-527A-21  |
| 5          | 77    | 9.6         | 1005   | 7     | US-11-113-424-63   |
| 6          | 76.5  | 9.5         | 833    | 7     | US-11-076-187-5    |
| 7          | 73    | 9.1         | 260    | 7     | US-11-182-946-8    |
| 8          | 71    | 8.8         | 164    | 6     | US-10-131-826A-314 |
| 9          | 70    | 8.7         | 3002   | 6     | US-10-821-234-916  |
| 10         | 68    | 8.5         | 451    | 7     | US-11-102-240-82   |
| 11         | 67    | 8.3         | 504    | 6     | US-10-999-782-2    |
| 12         | 66.5  | 8.3         | 283    | 6     | US-10-987-663-4    |
| 13         | 66    | 8.2         | 235    | 7     | US-11-126-126-16   |
| 14         | 66    | 8.2         | 461    | 7     | US-11-132-285-6    |
| 15         | 66    | 8.2         | 461    | 7     | US-11-182-946-4    |
| 16         | 65    | 8.1         | 1213   | 7     | US-11-039-398-14   |
| 17         | 65    | 8.1         | 1219   | 7     | US-11-039-398-10   |
| 18         | 65    | 8.1         | 1232   | 7     | US-11-039-398-18   |
| 19         | 65    | 8.1         | 1249   | 7     | US-11-039-398-22   |
| 20         | 64    | 8.0         | 172    | 6     | US-10-821-234-1272 |
| 21         | 64    | 8.0         | 4655   | 6     | US-10-995-561-556  |
| 22         | 63.5  | 7.9         | 237    | 6     | US-10-967-527A-17  |
| 23         | 63.5  | 7.9         | 816    | 7     | US-11-090-439-48   |
| 24         | 63.5  | 7.9         | 1036   | 6     | US-10-131-826A-142 |
| 25         | 63    | 7.8         | 2764   | 6     | US-10-995-561-691  |

|    |      |     |      |   |                    |                    |
|----|------|-----|------|---|--------------------|--------------------|
| 26 | 63   | 7.8 | 2813 | 6 | US-10-995-561-688  | Sequence 688, App  |
| 27 | 63   | 7.8 | 2919 | 6 | US-10-821-234-1133 | Sequence 1133, App |
| 28 | 63   | 7.8 | 5179 | 7 | US-11-108-172-1068 | Sequence 1068, App |
| 29 | 62.5 | 7.8 | 184  | 6 | US-10-742-634-9    | Sequence 9, Appli  |
| 30 | 62.5 | 7.8 | 184  | 6 | US-10-967-527A-8   | Sequence 8, Appli  |
| 31 | 62   | 7.7 | 838  | 6 | US-10-645-441-9    | Sequence 9, Appli  |
| 32 | 62   | 7.7 | 997  | 7 | US-11-113-424-37   | Sequence 37, Appli |
| 33 | 62   | 7.7 | 4419 | 6 | US-10-821-234-1155 | Sequence 1155, App |
| 34 | 62   | 7.7 | 5405 | 7 | US-11-108-172-1116 | Sequence 1116, App |
| 35 | 61.5 | 7.7 | 497  | 6 | US-10-821-234-1119 | Sequence 1119, App |
| 36 | 61.5 | 7.7 | 504  | 6 | US-10-763-712A-78  | Sequence 78, Appli |
| 37 | 61   | 7.6 | 755  | 7 | US-11-067-121-6    | Sequence 6, Appli  |
| 38 | 61   | 7.6 | 843  | 6 | US-10-645-441-7    | Sequence 7, Appli  |
| 39 | 61   | 7.6 | 843  | 6 | US-10-645-441-8    | Sequence 8, Appli  |
| 40 | 60.5 | 7.5 | 126  | 7 | US-11-113-424-184  | Sequence 184, App  |
| 41 | 60.5 | 7.5 | 349  | 7 | US-11-182-946-13   | Sequence 13, Appli |
| 42 | 60.5 | 7.5 | 598  | 7 | US-11-082-389-398  | Sequence 398, App  |
| 43 | 60.5 | 7.5 | 783  | 7 | US-11-186-284-59   | Sequence 59, Appli |
| 44 | 60.5 | 7.5 | 3690 | 6 | US-10-995-561-1016 | Sequence 1016, App |
| 45 | 60.5 | 7.5 | 3714 | 6 | US-10-995-561-1015 | Sequence 1015, App |

ALIGNMENTS

RESULT 1  
US-10-967-527A-19  
; Sequence 19, Application US/10967527A  
; Publication No. US20050256041A1  
; GENERAL INFORMATION:  
; APPLICANT: Fox, Brian A.  
; APPLICANT: Holloway, James L.  
; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor Receptor  
; TITLE OF INVENTION: Receptor  
; FILE REFERENCE: 03-17  
; CURRENT APPLICATION NUMBER: US/10/967,527A  
; PRIOR FILING DATE: 2004-10-18  
; PRIOR APPLICATION NUMBER: 60/511,698  
; PRIOR FILING DATE: 2003-10-16  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 292  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-967-527A-19

|                       |       |                       |                    |                                      |
|-----------------------|-------|-----------------------|--------------------|--------------------------------------|
| Query Match           | 24.8% | Score 199.5;          | DB 6;              | Length 292;                          |
| Best Local Similarity | 27.1% | Pred. No. 6.6e-13;    |                    |                                      |
| Matches               | 62;   | Conservative          | 10;                | Mismatches 52; Indels 105; Gaps 6;   |
| QY                    | 1     | MRSCPBEQYWAALLGTCMFC  | AI                 | CNHQSORTCAASC-----GEFWDLSFGDSVITP 51 |
| Db                    | 31    | MRSCPBEQYWDPLLGTCMCKT | CNHQSORTCAAF       | CRSLSCRKEQKGYDHLRLDCISA 90           |
| QY                    | 52    | NACPOS-----           | TLWPHSQVAER        | MAGGDVQ-----76                       |
| Db                    | 91    | SICGQHPKQCAVPCENKLR   | SPVNLPELR-----     | QRSGEVENNSDGRVQGLEHRSSEA 146         |
| QY                    | 77    | -----                 | CGTSYFSTFLLWPHCLLS | VSVMFPCSSLPVRL-----107               |
| Db                    | 147   | SPALPGLKLSADQVALVYST  | GLCLCAVLCCFLVAVAC  | FLKRGDPCSCQPRSRPRQSPA 206            |
| QY                    | 108   | -----                 | CTCCSRCLCMLSIIF    | PPQLPPTQLSGLGP 136                   |
| Db                    | 207   | KSSQDHAMEAGSPVSTSP    | BPVETCSFC-----     | FFCRAPTQESAVTP 247                   |

RESULT 2  
US-10-742-634-7  
; Sequence 7, Application US/10742634  
; Publication No. US20050249671A9

```

; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokinine-alpha Conjugate, Neutrokinine-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      24.3%; Score 195; DB 6; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.8e-12;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY      1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
Db      31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFRCISCRKEQKFDYDHLRLDSCA 90
QY      52 NACPQS-----TLPHSQVAERMAAGDVQ-----
Db      91 SICGHPKQCAVFCENKLRSPVNLPPELR---RQRSGEVNNSDNGRYQGLEHRGSEA 146
QY      77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPVL----- 107
Db      147 SPALPGLKLSAQVALVYTLGCLCAVLCCFLVAVACFLKKGDPCCQPRSRPRQSPA 206
QY      108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVTSPEPVEVCSPC-----PPECRAPTQESAVTP 248

RESULT 3
US-10-967-527A-20
; Sequence 20, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 48
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(48)
; OTHER INFORMATION: cysteine rich
US-10-967-527A-20

Query Match      22.4%; Score 180; DB 6; Length 48;
Best Local Similarity 86.1%; Pred. No. 1.1e-11;
Matches 31; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

; GENERAL INFORMATION:
; APPLICANT: Parmelee, David
; APPLICANT: Yeh, Ren-Hwa
; APPLICANT: Galperina, Olga
; APPLICANT: Hilbert, David
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Neutrokinine-alpha Conjugate, Neutrokinine-alpha Complex, and Uses Th
; FILE REFERENCE: 1488.1810002
; CURRENT APPLICATION NUMBER: US/10/742,634
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 60/435,262
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/467,198
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-742-634-7

Query Match      24.3%; Score 195; DB 6; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.8e-12;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY      1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
Db      31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFRCISCRKEQKFDYDHLRLDSCA 90
QY      52 NACPQS-----TLPHSQVAERMAAGDVQ-----
Db      91 SICGHPKQCAVFCENKLRSPVNLPPELR---RQRSGEVNNSDNGRYQGLEHRGSEA 146
QY      77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPVL----- 107
Db      147 SPALPGLKLSAQVALVYTLGCLCAVLCCFLVAVACFLKKGDPCCQPRSRPRQSPA 206
QY      108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVTSPEPVEVCSPC-----PPECRAPTQESAVTP 248

RESULT 5
US-11-113-424-63
; Sequence 63, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
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QY      1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC 36
Db      10 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAPC 45

RESULT 4
US-10-967-527A-21
; Sequence 21, Application US/10967527A
; Publication No. US20050256041A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Brian A.
; APPLICANT: Holloway, James L.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Ztnfr14, A Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor
; FILE REFERENCE: 03-17
; CURRENT APPLICATION NUMBER: US/10/967,527A
; CURRENT FILING DATE: 2004-10-18
; PRIOR APPLICATION NUMBER: 60/511,698
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 249
; TYPE: PRT
; ORGANISM: mus musculus
US-10-967-527A-21

Query Match      13.4%; Score 107.5; DB 6; Length 249;
Best Local Similarity 32.3%; Pred. No. 0.00051;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

QY      1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFMDLSPGDSVITP 51
Db      3 MAFCPKQYWDWSRKSVCSCALTCRSORSORTCTDFCKFNCRKEQGRYYDHLGACVSCD 62
QY      52 NACPQ 56
Db      63 STCTQ 67
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RESULT 5
US-11-113-424-63
; Sequence 63, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
```



```

; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 314
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-314

Query Match      8.8%; Score 71; DB 6; Length 164;
Best Local Similarity 24.7%; Pred. No. 1.2;
Matches 24; Conservative 7; Mismatches 30; Indels 36; Gaps 5;

Qy 14 LGTCMFCKAICNHOSQRTCAASCGBEFVDLSPGDSVITPNACPQSTLWPHSQVAERMAAG 73
Db 67 LGAICYCDLFCN---RTVSDCCPDFDFCLG---VPPPPPP-----IQGCMHGG 109

Qy 74 DVQCGTSPSTFLWPHCLLSVSNMPCSSLPRVLCCTC 110
Db 110 RI-----YPVLGTYWDNC-----NRCTC 127

RESULT 9
US-10-821-234-916
; Sequence 916, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821.234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 916
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-916

Query Match      8.7%; Score 70; DB 6; Length 3002;
Best Local Similarity 22.1%; Pred. No. 20;
Matches 33; Conservative 11; Mismatches 53; Indels 52; Gaps 8;

Ov 15 GTCMFCKAICNHOSQRTCAASCGBFWD-----LSPGDSVI 49

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCKATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCKGKTCNPRDSKYCEFDKACDNLCSNHGICTLGSQCDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTGTSYPSFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCLCML 119
DB 330 CVAQYSEEVCSNGEVCVG-----KCQAKVKGKNETYAGVFCDCNDCQSKYC 378
QY 120 SIIFPOLPPTQLSGL 134
DB 379 KALEPNVECNVIGQL 393

RESULT 12
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match
Best Local Similarity 8.3%; Score 66.5; DB 6; Length 283;
Matches 24; Conservative 7; Mismatches 49; Indels 15; Gaps 3;

QY 4 CPBEEQYWAAL--LGTCMFCKAI-----CNHQSQRTCAASCGFWDLSPGDSVIT 50
DB 78 CPPTGYIAHNLGSLKLCQCMCDPANGLRASRNCSTRTENAVCGSPGHFCIVQGDHCAA 137
QY 51 PNACPOSTLWPHSQVAEREMAGDVQCCTGTSYPSFTF 85
DB 138 CRAYATSS--PGQVQKGTESQDTLCQNCPPGTF 170

RESULT 13
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCKATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCKGKTCNPRDSKYCEFDKACDNLCSNHGICTLGSQCDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTGTSYPSFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCLCML 119
DB 330 CVAQYSEEVCSNGEVCVG-----KCQAKVKGKNETYAGVFCDCNDCQSKYC 378
QY 120 SIIFPOLPPTQLSGL 134
DB 379 KALEPNVECNVIGQL 393

RESULT 12
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match
Best Local Similarity 8.3%; Score 66.5; DB 6; Length 283;
Matches 24; Conservative 7; Mismatches 49; Indels 15; Gaps 3;

QY 4 CPBEEQYWAAL--LGTCMFCKAI-----CNHQSQRTCAASCGFWDLSPGDSVIT 50
DB 78 CPPTGYIAHNLGSLKLCQCMCDPANGLRASRNCSTRTENAVCGSPGHFCIVQGDHCAA 137
QY 51 PNACPOSTLWPHSQVAEREMAGDVQCCTGTSYPSFTF 85
DB 138 CRAYATSS--PGQVQKGTESQDTLCQNCPPGTF 170

RESULT 13
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCKATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCKGKTCNPRDSKYCEFDKACDNLCSNHGICTLGSQCDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTGTSYPSFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCLCML 119
DB 330 CVAQYSEEVCSNGEVCVG-----KCQAKVKGKNETYAGVFCDCNDCQSKYC 378
QY 120 SIIFPOLPPTQLSGL 134
DB 379 KALEPNVECNVIGQL 393

RESULT 12
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match
Best Local Similarity 8.3%; Score 66.5; DB 6; Length 283;
Matches 24; Conservative 7; Mismatches 49; Indels 15; Gaps 3;

QY 4 CPBEEQYWAAL--LGTCMFCKAI-----CNHQSQRTCAASCGFWDLSPGDSVIT 50
DB 78 CPPTGYIAHNLGSLKLCQCMCDPANGLRASRNCSTRTENAVCGSPGHFCIVQGDHCAA 137
QY 51 PNACPOSTLWPHSQVAEREMAGDVQCCTGTSYPSFTF 85
DB 138 CRAYATSS--PGQVQKGTESQDTLCQNCPPGTF 170

RESULT 13
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCKATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCKGKTCNPRDSKYCEFDKACDNLCSNHGICTLGSQCDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTGTSYPSFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCLCML 119
DB 330 CVAQYSEEVCSNGEVCVG-----KCQAKVKGKNETYAGVFCDCNDCQSKYC 378
QY 120 SIIFPOLPPTQLSGL 134
DB 379 KALEPNVECNVIGQL 393

RESULT 12
US-10-987-663-4
; Sequence 4, Application US/10987663
; Publication No. US20050272118A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: CLARK, HILARY
; APPLICANT: EATON, DANIEL L.
; APPLICANT: WRANIK, BERND
; APPLICANT: OUYANG, WENJUN
; APPLICANT: GONZALES, LINO
; APPLICANT: LOYET, KELLY M.
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of
; TITLE OF INVENTION: Immune Related Diseases
; FILE REFERENCE: P1996R1P1-US
; CURRENT APPLICATION NUMBER: US/10/987,663
; CURRENT FILING DATE: 2004-11-12
; PRIOR APPLICATION NUMBER: US 60/421,236
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 10/371,341
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-987-663-4

Query Match
Best Local Similarity 8.3%; Score 66.5; DB 6; Length 283;
Matches 24; Conservative 7; Mismatches 49; Indels 15; Gaps 3;

QY 4 CPBEEQYWAAL--LGTCMFCKAI-----CNHQSQRTCAASCGFWDLSPGDSVIT 50
DB 78 CPPTGYIAHNLGSLKLCQCMCDPANGLRASRNCSTRTENAVCGSPGHFCIVQGDHCAA 137
QY 51 PNACPOSTLWPHSQVAEREMAGDVQCCTGTSYPSFTF 85
DB 138 CRAYATSS--PGQVQKGTESQDTLCQNCPPGTF 170

RESULT 13
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-999-782-2

Query Match
Best Local Similarity 8.3%; Score 67; DB 6; Length 504;
Matches 30; Conservative 14; Mismatches 65; Indels 26; Gaps 5;

QY 15 GTCMFCKATCNHQ-----SQRTCAASCGFWDLSPG-----DSVITPN--ACPOSTLW 60
DB 270 GVMCKGKTCNPRDSKYCEFDKACDNLCSNHGICTLGSQCDSGWSGNDGCGPTNTD 329
QY 61 PHSQVAEREMAG-GDVQCCTGTSYPSFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCL
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; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2

Query Match      24.3%; Score 195; DB 2; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.4e-11;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy      1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51
Db      31 MRSCPEQYWDPLLTGTCMSKTCICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
Qy      52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76
Db      91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
Qy      77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107
Db      147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCQCPQSRPRQSPA 206
Qy      108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVSTSPBVTCSFC-----FPFCRAPTQESAVTP 248

RESULT 5
US-09-879-919-22
; Sequence 22, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13

Query Match      24.3%; Score 195; DB 2; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.4e-11;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy      1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51
Db      31 MRSCPEQYWDPLLTGTCMSKTCICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
Qy      52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76
Db      91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
Qy      77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107
Db      147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCQCPQSRPRQSPA 206
Qy      108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVSTSPBVTCSFC-----FPFCRAPTQESAVTP 248

RESULT 6
US-09-848-295-4
; Sequence 4, Application US/09848295
; Patent No. 6623941
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
; TITLE OF INVENTION: Thereon
; FILE REFERENCE: PF527
; CURRENT APPLICATION NUMBER: US/09/848,295
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,193
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-848-295-4

Query Match      24.3%; Score 195; DB 2; Length 293;
Best Local Similarity 27.0%; Pred. No. 1.4e-11;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy      1 MRSCPEQYWAALGTGCMCKAICNHQSORTCAASC-----GFWDLSPGDSVITP 51
Db      31 MRSCPEQYWDPLLTGTCMSKTCICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
Qy      52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76
Db      91 SICGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
Qy      77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107
Db      147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCQCPQSRPRQSPA 206
Qy      108 -----CTCCSRCLCMLSIIPQL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVSTSPBVTCSFC-----FPFCRAPTQESAVTP 248
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Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSRPRQSPA 206  
QY 108 -----CTCSRCLCMLSIIPQL-PPQLSGLGP 136  
Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----PPECRAPTQESAVTP 248  
RESULT 7  
US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE REFERENCE: BLYS/AGP-3, AND TACI  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14  
Query Match 24.3%; Score 195; DB 2; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.4e-11;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
QY 1 MRSCEPYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCEPYWDPLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPOS -----TLWPHSQVAERMGAGDVQ----- 76  
Db 91 SICGHPKQCAYPENKLRSPVNLPELR-----QRSGEVNNDSNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPVYL----- 107  
Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSRPRQSPA 206  
QY 108 -----CTCSRCLCMLSIIPQL-PPQLSGLGP 136  
Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----PPECRAPTQESAVTP 248  
RESULT 8  
US-08-810-572A-6  
; Sequence 6, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; FLOOR: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-810-572A-6  
Query Match 24.0%; Score 192.5; DB 1; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCEPYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCEPYWDPLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95  
RESULT 9  
US-09-290-333-6  
; Sequence 6, Application US/09290333  
; Patent No. 6316222  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; FLOOR: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/290,333  
; FILING DATE: 12-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-290-333-6

Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLLTGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 10  
US-09-782-857A-6  
Sequence 6, Application US/09782857A  
Patent No. 6500428  
GENERAL INFORMATION:  
APPLICANT: Bram, Richard J.  
von Bulow, Gotz  
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
THEREOF  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/782,857A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/810,572  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1340-1-007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 166 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
FRAGMENT TYPE: N-terminal  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-782-857A-6  
Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLLTGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 11  
US-09-854-864-15  
Sequence 15, Application US/09854864  
Patent No. 6774106  
GENERAL INFORMATION:  
APPLICANT: THEILL, LARS EYDE  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591  
PRIOR FILING DATE: 2000-06-27  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 166  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-854-864-15

Query Match 24.0%; Score 192.5; DB 2; Length 166;  
Best Local Similarity 56.9%; Pred. No. 1.3e-11;  
Matches 37; Conservative 4; Mismatches 15; Indels 9; Gaps 1;  
QY 1 MRSCPPEQYWAALLGTCMCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
Db 31 MRSCPPEQYWDPLLTGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQ 56  
Db 91 SICGQ 95

RESULT 12  
US-09-854-864-18  
Sequence 18, Application US/09854864  
Patent No. 6774106  
GENERAL INFORMATION:  
APPLICANT: THEILL, LARS EYDE  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
FILE REFERENCE: A-686B  
CURRENT APPLICATION NUMBER: US/09/854,864  
CURRENT FILING DATE: 2001-09-11  
PRIOR APPLICATION NUMBER: US 60/204,039  
PRIOR FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: US 60/214,591

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; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-18

Query Match      24.0%; Score 192.5; DB 2; Length 397;
Best Local Similarity 56.9%; Pred. No. 3.5e-11;
Matches 3; Conservative 4; Mismatches 15; Indels 9; Gaps 1;

QY 1 MRSPPEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51
Db 31 MRSPPEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90

QY 52 NACPQ 56
Db 91 SICGQ 95

RESULT 13
US-09-854-864-16
; Sequence 16, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-16

Query Match      22.5%; Score 180.5; DB 2; Length 67;
Best Local Similarity 58.6%; Pred. No. 7.3e-11;
Matches 34; Conservative 4; Mismatches 15; Indels 5; Gaps 1;

QY 4 CPBEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNACPQ 56
Db 1 CPBEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCAICQ 58

RESULT 14
US-09-854-864-20
; Sequence 20, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; FILE REFERENCE: BLYS/AGP-3, AND TACI
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 20
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-20

Query Match      21.5%; Score 172.5; DB 2; Length 59;
Best Local Similarity 66.0%; Pred. No. 4e-10;
Matches 31; Conservative 2; Mismatches 5; Indels 9; Gaps 1;

QY 4 CPBEQYWAALIGTCMFCCKAICNHQSORTCAASC-----GEFWD 41
Db 1 CPBEQYWDPLIGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYD 47

RESULT 15
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-286-529-17

Query Match      11.9%; Score 95.5; DB 2; Length 299;
Best Local Similarity 25.4%; Pred. No. 0.11;
Matches 36; Conservative 9; Mismatches 46; Indels 51; Gaps 7;

QY 4 CPBE-----QYWAALIGTCMFCCKAICNHQSQ--RTCAAS-----CGEFWD 41
Db 73 CPPRHYTQFW-NYLERCRYCNVLCGEREBEARACHATHNRACRGTGFFAHAGFCLHAS 131

QY 42 LSPGDSVITPNACPOSTLWPHSQVAERMAAGDVCGTGVPSSTF-----LLWPH--- 90
Db 132 CPPGAGVIAPGTPTSQNT-----QQPCPPGTFSASSSSSEQCPHFNCT 174

QY 91 CLLSVSNMPCSSLPRVLCTCCS 112
Db 175 ALGLALNVFGSSSHDTLCTSCT 196

Search completed: December 20, 2005, 10:34:28
Job time : 47 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:33 ; Search time 185 Seconds

(without alignments)  
337.253 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

Sequence: 1 MRSCPQQWAAALLGTCMFC.....FPQLPPTQLSGLPNIGGLL 142

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A Geneseq 21:\*

1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*  
9: Geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 803   | 100.0       | 142    | 7  | Adf77377 Human tum |
| 2          | 803   | 100.0       | 142    | 8  | Adj92512 Human TR2 |
| 3          | 697.5 | 86.9        | 154    | 5  | Aae29295 Human gen |
| 4          | 199.5 | 24.8        | 292    | 9  | Adz67771 Human tum |
| 5          | 198.5 | 24.7        | 291    | 5  | Aau10949 Human AGP |
| 6          | 198   | 24.7        | 293    | 5  | Aau09900 Human AGP |
| 7          | 195   | 24.3        | 265    | 4  | Aae09244 Human TAC |
| 8          | 195   | 24.3        | 266    | 6  | Abp97723 Amino aci |
| 9          | 195   | 24.3        | 266    | 9  | Adw03442 Human TAC |
| 10         | 195   | 24.3        | 293    | 2  | Aaw75783 Human lym |
| 11         | 195   | 24.3        | 293    | 3  | Abb36312 Human neu |
| 12         | 195   | 24.3        | 293    | 3  | Aay94000 A transme |
| 13         | 195   | 24.3        | 293    | 4  | Aae09240 Human TAC |
| 14         | 195   | 24.3        | 293    | 4  | Aay71914 Human tum |
| 15         | 195   | 24.3        | 293    | 5  | Aao14130 Human tra |
| 16         | 195   | 24.3        | 293    | 5  | Abb81488 Human TAC |
| 17         | 195   | 24.3        | 293    | 5  | Aau99512 Human TAC |
| 18         | 195   | 24.3        | 293    | 5  | Aae28962 Human TAC |
| 19         | 195   | 24.3        | 293    | 5  | Aau75408 Tumour ne |
| 20         | 195   | 24.3        | 293    | 5  | Aae15493 Human tra |
| 21         | 195   | 24.3        | 293    | 5  | Abg71496 Human tum |
| 22         | 195   | 24.3        | 293    | 6  | Aae35211 Human TAC |
| 23         | 195   | 24.3        | 293    | 6  | Abp60551 Human tum |
| 24         | 195   | 24.3        | 293    | 6  | Abp97716 Amino aci |

|    |       |      |     |   |          |           |
|----|-------|------|-----|---|----------|-----------|
| 25 | 195   | 24.3 | 293 | 6 | AAO29592 | Human DIT |
| 26 | 195   | 24.3 | 293 | 7 | Adf72628 | Human tum |
| 27 | 195   | 24.3 | 293 | 7 | Adf77379 | Human tum |
| 28 | 195   | 24.3 | 293 | 7 | Abm85745 | Human pro |
| 29 | 195   | 24.3 | 293 | 8 | Adk00754 | Native hu |
| 30 | 195   | 24.3 | 293 | 8 | Adj92514 | Human TAC |
| 31 | 195   | 24.3 | 293 | 8 | Adn03174 | Human TAC |
| 32 | 195   | 24.3 | 293 | 8 | Adq76815 | Human TAC |
| 33 | 195   | 24.3 | 293 | 8 | Adq94440 | Neutrokin |
| 34 | 195   | 24.3 | 293 | 9 | Adw03430 | Human TAC |
| 35 | 195   | 24.3 | 294 | 9 | Adw03443 | Human TAC |
| 36 | 195   | 24.3 | 312 | 5 | AAO14135 | Protein o |
| 37 | 194   | 24.2 | 294 | 8 | Adk00765 | htACI spl |
| 38 | 193   | 24.0 | 344 | 6 | AAE35224 | Human TAC |
| 39 | 192.5 | 24.0 | 166 | 2 | AAW75785 | Human lym |
| 40 | 192.5 | 24.0 | 166 | 5 | AAE15494 | Human TAC |
| 41 | 192.5 | 24.0 | 171 | 8 | Adn03188 | Human TAC |
| 42 | 192.5 | 24.0 | 332 | 6 | AAE35228 | Human TAC |
| 43 | 192.5 | 24.0 | 348 | 6 | AAE35225 | Human TAC |
| 44 | 192.5 | 24.0 | 357 | 6 | AAE35226 | Human TAC |
| 45 | 192.5 | 24.0 | 366 | 5 | AAO14132 | Protein o |

## ALIGNMENTS

RESULT 1

ADf77377  
ID ADf77377 standard; protein; 142 AA.

XX ADf77377;

DT 26-FEB-2004 (first entry)

DE Human tumour necrosis factor receptor TR20.

XX Human; tumour necrosis factor receptor; TR20; receptor; gene therapy;  
KW B cell; cell survival; upregulated cell proliferation; apoptosis; cancer;  
KW autoimmune disease; viral infection; inflammation;  
KW graft-versus-host disease; acute graft rejection;  
KW chronic graft rejection; AIDS; neurodegenerative disorder;  
KW myelodysplastic syndromes; ischaemic injury; toxin-induced liver disease;  
KW septic shock; cachexia; anorexia.

XX Homo sapiens.

| Key       | Location/Qualifiers                                      |
|-----------|--|
| FT Region | 1..142   |
| FT Domain | /note= "This region is specifically claimed in claim 39" |
| FT Domain | /label = Extracellular domain                            |
| FT Region | /note= "This region is specifically claimed in claim 39" |
| FT Region | /note= "This region is specifically claimed in claim 1"  |
| FT Region | /note= "This region is specifically claimed in claim 1"  |
| FT Region | /note= "This region is specifically claimed in claim 1"  |
| FT Domain | /note= "This region is specifically claimed in claim 1"  |
| FT Domain | /label = Intracellular domain                            |
| FT Domain | /note= "This region is specifically claimed in claim 39" |

US6623941-B1.

23-SEP-2003.

04-MAY-2001; 2001US-00848295.

05-MAY-2000; 2000US-0202193P.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Baker KP, Ni J;

XX WPI; 2003-895467/82.  
 DR N-PSDB; ADF77376.  
 XX  
 XX New TR20 nucleic acid molecules, useful for treating diseases associated  
 PT with increased cell survival, upregulated cell proliferation, or  
 PT inhibition of apoptosis, e.g. cancer, autoimmune diseases, viral  
 PT infections, inflammation.  
 XX  
 XX Claim 1; SEQ ID NO 2; 102pp; English.  
 PS  
 CC The invention relates to an isolated nucleic acid molecule consisting of  
 CC a sequence that is at least 90% identical to a sequence encoding Human  
 CC tumour necrosis factor receptor (TR20) polypeptide (appearing as  
 CC ADF77377) or its fragments, complement, and optionally a heterologous  
 CC nucleic acid sequence that is preferentially expressed in mature B cells.  
 CC Also included are a method of making a recombinant vector by inserting  
 CC the nucleic acid molecule into a vector, a recombinant vector produced by  
 CC the method, a method of making a recombinant host cell by introducing the  
 CC recombinant vector into a cell, a recombinant host cell produced by the  
 CC method and a recombinant method of producing a polypeptide by culturing  
 CC the recombinant host cell under conditions where the polypeptide is  
 CC expressed and recovering the polypeptide. The nucleic acid molecules are  
 CC useful for treating diseases associated with increased cell survival,  
 CC upregulated cell proliferation, or inhibition of apoptosis, e.g. cancer,  
 CC autoimmune diseases, viral infections, inflammation, graft-versus-host  
 CC disease, acute graft rejection, chronic graft rejection, AIDS,  
 CC neurodegenerative disorders, myelodysplastic syndromes, ischaemic injury,  
 CC toxin-induced liver disease, septic shock, cachexia, and anorexia. The  
 CC present sequence represents human TR20.  
 XX  
 SQ Sequence 142 AA;  
 Query Match 100.0%; Score 803; DB 7; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 38-69;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASCGEFWDLSPGDSVITPNACPOSTLW 60  
 DB 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASCGEFWDLSPGDSVITPNACPOSTLW 60  
 QY 61 PHSQVAERWAGDVCGTGYPTFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCRLCMLS 120  
 DB 61 PHSQVAERWAGDVCGTGYPTFTLLWPHCLLSVSNMPCSSLPRVLCTCCSCRLCMLS 120  
 QY 121 IIFPQLPPTQLSLGPNIGLL 142  
 DB 121 IIFPQLPPTQLSLGPNIGLL 142  
 RESULT 2  
 ADJ92512  
 ID ADJ92512 standard; protein; 142 AA.  
 XX  
 AC ADJ92512;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human TR20.  
 XX  
 KW human; TR20; immunodeficiency; autoimmune disease;  
 KW severe combined immunodeficiency; SCID-X linked; SCID-autosomal;  
 KW adenosine deaminase deficiency; ADA deficiency;  
 KW X-linked agammaglobulinemia; XLA; Bruton's disease;  
 KW congenital agammaglobulinemia; X-linked infantile agammaglobulinemia;  
 KW acquired agammaglobulinemia; adult onset agammaglobulinemia;  
 KW late-onset agammaglobulinemia; dysagammaglobulinemia;  
 KW hypogammaglobulinemia; transient hypogammaglobulinemia of infancy;  
 KW unspecified hypogammaglobulinemia; agammaglobulinemia;  
 KW common variable immunodeficiency; CVID; Wiskott-Aldrich Syndrome; WAS;  
 KW selective IgA deficiency; B cell lymphoproliferative disorder; BLPD;  
 KW recessive agammaglobulinemia; reticular dysgenesis;  
 KW neonatal neutropenia; severe congenital leukopenia;

thymic lymphoplasia-aplasia; ataxia-telangiectasia;  
 short limbed dwarfism; X-linked lymphoproliferative syndrome; XLP;  
 purine nucleoside phosphorylase; PNP deficiency; MHC Class II deficiency;  
 Bare Lymphocyte Syndrome; autoimmune haemolytic anaemia;  
 autoimmune neonatal thrombocytopenia;  
 idiopathic thrombocytopenia purpura; autoimmune thrombocytopenia;  
 autoimmune neutropenia; haemolytic anaemia; antiphospholipid syndrome;  
 dermatitis; allergic encephalomyelitis; myocarditis;  
 relapsing polychondritis; rheumatic heart disease; glomerulonephritis;  
 Multiple Sclerosis; Neuritis; Uveitis Ophthalmia; Polyendocrinopathy;  
 Purpura; Stiff-Man Syndrome; Autoimmune Pulmonary Inflammation;  
 Guillain-Barre Syndrome; insulin dependent diabetes mellitus;  
 juvenile onset diabetes; autoimmune thyroiditis; hypothyroidism;  
 receptor autoimmunity; autoimmune thrombotic purpura;  
 rheumatoid arthritis; gluten-sensitive enteropathy;  
 dense deposit disease; scleroderma; mixed connective tissue disease;  
 polymyositis; dermatomyositis; pernicious anaemia; infertility;  
 glomerulonephritis; bullous pemphigoid; Sjogren's syndrome;  
 diabetes mellitus; chronic active hepatitis; primary biliary cirrhosis;  
 vitiligo; vasculitis; cardiomyopathy; urticaria; atopic dermatitis;  
 asthma; inflammatory myopathy; inflammatory skin disease; psoriasis;  
 sclerosis; inflammatory bowel disease; Crohn's disease;  
 ulcerative colitis; respiratory distress syndrome;  
 adult respiratory distress syndrome; ARDS; meningitis; encephalitis;  
 colitis; allergy; eczema.  
 Homo sapiens.  
 US2004048296-A1.  
 11-MAR-2004.  
 15-JUL-2003; 2003US-00618797.  
 05-MAY-2000; 2000US-0202193P.  
 04-MAY-2001; 2001US-00848295.  
 (HUMA-) HUMAN GENOME SCI INC.  
 Ruben SM, Baker KP, N1 J;  
 WPI; 2004-226194/21.  
 N-PSDB; ADJ92511.  
 New isolated human tumor necrosis factor TR20 polypeptide and nucleic  
 acid molecule, useful for diagnosing or treating conditions with aberrant  
 expression of the TR20 polypeptide, such as immunodeficiency and  
 autoimmune diseases.  
 Disclosure; SEQ ID NO 2; 114pp; English.  
 The invention relates to an isolated nucleic acid. The nucleic acid and  
 its protein are useful for the diagnosis and/or treatment of  
 immunodeficiency and/or autoimmune diseases or conditions associated with  
 aberrant expression or activity of the TR20 polypeptide, such as severe  
 combined immunodeficiency (SCID)-X linked, SCID-autosomal, adenosine  
 deaminase deficiency (ADA deficiency), X-linked agammaglobulinemia  
 (XLA), Bruton's disease, congenital agammaglobulinemia, X-linked  
 infantile agammaglobulinemia, acquired agammaglobulinemia, adult onset  
 agammaglobulinemia, late-onset agammaglobulinemia,  
 dysagammaglobulinemia, hypogammaglobulinemia, transient  
 hypogammaglobulinemia of infancy, unspecified hypogammaglobulinemia,  
 agammaglobulinemia, common variable immunodeficiency (CVID), Wiskott-  
 Aldrich Syndrome (WAS), X-linked immunodeficiency with hyper IgM, non X-  
 linked immunodeficiency with hyper IgM, selective IgA deficiency, IGG  
 subclass deficiency (with or without IgA deficiency), antibody deficiency  
 with normal or elevated Igs, immunodeficiency with thymoma, Ig heavy  
 chain deletions, kappa chain deficiency, B cell lymphoproliferative  
 disorder (BLPD), selective IgM immunodeficiency, recessive  
 agammaglobulinemia (Swiss type), reticular dysgenesis, neonatal  
 neutropenia, severe congenital leukopenia, thymic lymphoplasia-aplasia  
 or dysplasia with immunodeficiency, ataxia-telangiectasia, short limbed  
 dwarfism, X-linked lymphoproliferative syndrome (XLP), Nezelof syndrome-

```

Query Match      100.0%; Score 803; DB 8; Length 142;
Best Local Similarity 100.0%; Pred. No. 3e-69;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MRSCEPEQYWAALLGTCMFCFKAI CNHOSQRTCAASCGEFWDLSFGDSVITFNACPQSTLW 60
      |||||
Db       1  MRSCEPEQYWAALLGTCMFCFKAI CNHOSQRTCAASCGEFWDLSFGDSVITFNACPQSTLW 60
      |||||

QY      61  PHSQVAERMAGGVQCGTSPYFTLLMPHCLLSVSNMPCSSLPRVLCTCCSRCLECMLS 120
      |||||
Db       61  PHSQVAERMAGGVQCGTSPYFTLLMPHCLLSVSNMPCSSLPRVLCTCCSRCLECMLS 120
      |||||

QY      121 IIPQLPPTQLSGLGPNIGGL 142
      |||||
Db       121 IIPQLPPTQLSGLGPNIGGL 142
      |||||

RESULT 3
AAE29295
ID      AAE29295 standard; protein; 154 AA.
XX
AAE29295;
XX
XX
DT      27-JAN-2003 (first entry)
XX
XX      Human gene 6 encoded protein HPMKI40, SEQ ID NO:22.

```

QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNA 60  
 DB 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITPNA 60  
 QY 61 PHSQVAERWAGGVDVCGTSPSTFLWPHCLLSVSNMPCSSLPVLTCTCCSRCLCMLS 120  
 DB 61 PHSQVAERWAGGVDVCGTSPSTFLWPHCLLSVSNMPCSSLPVLTCTCCSRCLCMLS 120  
 QY 121 IIFPQLPPTQLSLGPN 137  
 DB 121 IIF-----LSXILPN 130

RESULT 4  
 ADZ67771  
 ID ADZ67771 standard; protein; 292 AA.  
 AC ADZ67771;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Human tumor necrosis factor receptor TACI.  
 XX  
 KW Tumor necrosis factor receptor; TACI; cancer; neoplasm; diagnosis;  
 KW cytosstatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Key Location/Qualifiers  
 FT Domain 22..43  
 FT /note= "Cys-rich domain"  
 XX  
 PN WO2005037865-A2.  
 XX  
 PD 28-APR-2005.  
 XX  
 PF 18-OCT-2004; 2004WO-US034375.  
 XX  
 PR 16-OCT-2003; 2003US-0511698P.  
 PR 18-OCT-2004; 2004US-0619552P.  
 XX  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Fox BA, Holloway JL, Sheppard PO, Dillon SR;  
 XX  
 DR WPI; 2005-315682/32.  
 XX  
 PT New tumor necrosis factor receptor (TNFR) polypeptides, useful as  
 PT detecting ligands, and for modulating tumor growth, metastasis and  
 PT immunity, such as separating resting from stimulated immune cells.  
 XX  
 PS Disclosure; SEQ ID NO 19; 132pp; English.  
 XX  
 CC The invention provides novel tumor necrosis factor receptor (TNFR)  
 CC znfr14 polynucleotides ADZ67753 and polypeptides ADZ67754, expression  
 CC vectors and antibodies. Znfr14 polynucleotides are used in claimed  
 CC methods for detecting a genetic abnormality in a patient and for  
 CC detecting a cancer in a patient. Recombinant znfr14 polypeptide,  
 CC optionally conjugated to a toxin, is used in a claimed method of killing  
 CC cancer cells. Znfr14 polypeptides can be used to detect ligands,  
 CC agonists and antagonists. The polypeptides, polynucleotides and  
 CC antibodies may also be used in methods that modulate tumor growth,  
 CC metastasis, and immunity such as separating resting from stimulated  
 CC immune cells. The present sequence is that of human TNFR TACI. This  
 CC sequence was compared with that of znfr14 in the identification of  
 CC znfr14 as a member of the TNFR family.  
 XX  
 SQ Sequence 292 AA;  
 Query Match 24.8%; Score 199.5; DB 9; Length 292;  
 Best Local Similarity 27.1%; Pred. No. 7.Be-11;  
 Matches 62; Conservative 10; Mismatches 52; Indels 105; Gaps 6;

QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 DB 31 MRSCPEQYWDPLLTGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQAERWAGGVDVQ----- 76  
 DB 91 SICGQHPKQCAYPECNKLRSPVNLPELR-----RQSGEVNNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSPSTFLWPHCLLSVSNMPCSSLPVLTCTCCSRCLCMLS 107  
 DB 147 SPALPGLKLSADQVALVYSTGLCLCAVLCLVAVACFLKRGDPCSCQPRRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFFQLPPTQLSLG 136  
 DB 207 KSSQDHAMEAGSPVSTSPBVTCSFC-----FFCRAPTQESAVTP 247

RESULT 5  
 AAU10949  
 ID AAU10949 standard; protein; 291 AA.  
 XX  
 AC AAU10949;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Human AGP-3 receptor extracellular domain.  
 XX  
 KW Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;  
 KW dermatological; neuroprotective; nootropic; immunomodulator; metabolic;  
 KW antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever;  
 KW antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma;  
 KW AGP-3 receptor; tumor necrosis factor ligand family; AGP-3 receptor;  
 KW mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder;  
 KW rheumatoid arthritis; graft-versus-host disease; Crohn's disease;  
 KW pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease;  
 KW diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;  
 KW multiple sclerosis; Parkinson's disease; transgenic animal.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO200185782-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 12-FEB-2001; 2001WO-US004568.  
 XX  
 PR 11-FEB-2000; 2000US-0181800P.  
 XX  
 XX (AMGE-) AMGEN INC.  
 PA  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2002-049441/06.  
 XX  
 PT Composition, useful for identifying modulator of receptor for treating  
 PT asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor  
 PT ligand family member) receptor and encoding nucleic acids.  
 XX  
 PS Claim 1; Fig 18; 124pp; English.  
 XX  
 CC The invention relates to a composition (I) comprising AGP-3 receptor  
 CC (tumor necrosis factor ligand family member) related protein (II)  
 CC attached to a vehicle protein. (I) is useful for modulating AGP-3-related  
 CC activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in  
 CC assays to identify cells and tissues that express AGP-3R or proteins  
 CC related to AGP-3-related protein and for identifying compounds (agonists  
 CC or antagonists) that interact with AGP-3R proteins. (I) is also useful  
 CC for identifying intracellular proteins that interact with the respective  
 CC cytoplasmic domains by yeast two-hybrid screening process. (II) is  
 CC involved in B cell growth, survival and activation particularly in lymph  
 CC node, spleen, and Peyer's patches. AGP-3R agonists and antagonists  
 CC identified using (II) are used for modulating B cell response and are  
 CC used to treat diseases characterised by inflammatory processes or



deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 extracellular domain

XX SQ Sequence 291 AA;

Query Match 24.7%; Score 198.5; DB 5; Length 291;  
Best Local Similarity 27.1%; Pred. No. 9.7e-11;  
Matches 62; Conservative 12; Mismatches 50; Indels 105; Gaps 7;  
QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWLSPQDSVITP 51  
Db 31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLPHSQVAERMGAGDVQ----- 76  
Db 91 SICGQHPKQCAVFCENKLRSPVNLPELR----RQRSGEVENNSDNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQAVVYSTGLCLCAVLCFLVAVACFLKMGDPCSCQPRSPROSPAK 206  
QY 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSGLGP 136  
Db 207 SSQDHAMEAGSPVSTSPVPETCSFC-----FPCECRAPTQESAVTP 247

RESULT 6  
AAU09900  
ID AAU09900 standard; protein; 293 AA.  
AC AAU09900;  
XX  
XX  
XX 12-MAR-2002 (first entry)  
XX Human AGP-3 related protein receptor.

XX Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive; dermatological; neuroprotective; nootropic; immunomodulator; metabolic; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antiparkinsonian; antipsoriatic; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancreatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.

XX Homo sapiens.

XX WO200185782-A2.

XX 15-NOV-2001.

XX 12-FEB-2001; 2001WO-US004568.

XX 11-FEB-2000; 2000US-0181800P.

XX (AMGE-) AMGEN INC.

PI Boyle WJ, Hsu H;  
XX WPI; 2002-049441/06.  
DR N-PSDB; AAS18558.  
XX

Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumour necrosis factor ligand family member) receptor and encoding nucleic acids.

XX Disclosure; Page 117-119; 124pp; English.

XX The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists identified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-host disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells which are derived from B cells, which involves treating the hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, diabetes, fever, glomerulonephritis, inflammatory bowel disease, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, pain, reperfusion injury, septic shock, etc. The nucleic acids are also useful for developing the transgenic animals expressing (II), which are useful for producing the polypeptides and for the study of in vivo biological activity. The present sequence represents the amino acid sequence of human AGP-3 related protein receptor

XX SQ Sequence 293 AA;

Query Match 24.7%; Score 198; DB 5; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.1e-10;  
Matches 62; Conservative 12; Mismatches 50; Indels 106; Gaps 7;

QY 1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWLSPQDSVITP 51  
Db 31 MRSCPEQYWDPLLGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLPHSQVAERMGAGDVQ----- 76  
Db 91 SICGQHPKQCAVFCENKLRSPVNLPELR----RQRSGEVENNSDNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRLV----- 107  
Db 147 SPALPGLKLSADQAVVYSTGLCLCAVLCFLVAVACFLKMGDPCSCQPRSPROSPA 206  
QY 108 -----CTCCSRCLCMLSIIFPOL-PPTQLSGLGP 136  
Db 207 KSSQDHAMEAGSPVSTSPVPETCSFC-----FPCECRAPTQESAVTP 248

RESULT 7  
AAE09244  
ID AAE09244 standard; protein; 265 AA.

XX AAE09244;

XX 19-NOV-2001 (first entry)

XX Human TACI splice variant protein.

XX Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.  
 XX Homo sapiens.  
 OS  
 PN WO200160397-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 28-NOV-2000; 2000WO-US032378.  
 XX  
 PR 16-FEB-2000; 2000US-0182938P.  
 XX  
 PR 22-AUG-2000; 2000US-0226986P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;  
 XX  
 DR WPI; 2001-541628/60.  
 XX  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.  
 XX  
 PS Example 1; Fig 6; 160pp; English.  
 XX  
 CC The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human TACI splice variant protein  
 XX  
 SQ Sequence 265 AA;  
 Query Match 24.3%; Score 195; DB 4; Length 265;  
 Best Local Similarity 27.0%; Pred. No. 1.9e-10;  
 Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
 QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 DB 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQAVERMAGDVQ----- 76  
 DB 91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLICLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLICLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 RESULT 8  
 ABP97723  
 ID ABP97723 standard; protein; 266 AA.  
 XX  
 AC ABP97723;  
 XX  
 XX 28-MAY-2003 (first entry)  
 DT  
 XX

DE Amino acid sequence of an alternatively spliced human TACI receptor.  
 XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003014294-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 24-JUL-2002; 2002WO-US023487.  
 XX  
 PR 03-AUG-2001; 2001US-0310114P.  
 XX  
 PR 30-APR-2002; 2002US-0377171P.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Dixit V, Grewal I, Ridgway J, Yan M;  
 PI WPI; 2003-256560/25.  
 XX  
 DR WPI; 2003-256560/25.  
 XX  
 XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.  
 PT  
 PS Disclosure; Fig 8; 153pp; English.  
 XX  
 CC The present sequence represents an alternatively spliced human TACI  
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and  
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and  
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also  
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful  
 CC for preparing a composition for treating systemic lupus erythematosus  
 XX  
 SQ Sequence 266 AA;  
 Query Match 24.3%; Score 195; DB 6; Length 266;  
 Best Local Similarity 27.0%; Pred. No. 1.9e-10;  
 Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
 QY 1 MRSCPEQYWAALLGTCMFCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 DB 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQAVERMAGDVQ----- 76  
 DB 91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPRVL----- 107  
 DB 147 SPALPGLKLSADQVALVYSTGLICLCAVLCCFLVAVACFLKKGDFCSCQPRSRPRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 DB 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PFECRAPTQESAVTP 248  
 RESULT 9  
 ADW03442  
 ID ADW03442 standard; protein; 266 AA.  
 XX  
 AC ADW03442;  
 XX  
 XX 24-MAR-2005 (first entry)  
 DT  
 XX  
 DE Human TACI protein amino acid sequence #3.  
 XX  
 KW B-lymphocyte; b-cell lymphoma; autoimmune disease; immunosuppressive;  
 KW non-hodgkin lymphoma; hodgkins disease; cytostatic;  
 KW chronic lymphocytic leukemia; hairy cell leukemia; rheumatoid arthritis;  
 KW antiarthritic; antirheumatic; systemic lupus erythematosus;  
 KW Wegener granulomatosis; anti-allergic; anti-inflammatory; vasotropic;  
 KW inflammatory bowel disease; gastrointestinal-gen.;

idiopathic thrombocytopenic purpura; hemostatic; multiple sclerosis; asthma; antiasthmatic; psoriasis; antipsoriatic; myasthenia gravis; muscular-gen.; neuroprotective; vasculitis; diabetes; antidiabetic; glomerulonephritis; nephrotropic; TACI.

Homo sapiens.  
W02005000351-A2.

06-JAN-2005.

04-JUN-2004; 2004WO-US017693.

05-JUN-2003; 2003US-0476414P.

05-JUN-2003; 2003US-0476481P.

06-JUN-2003; 2003US-0476531P.

(GETH ) GENENTECH INC.

Chan A, Gong Q, Martin F;

WPI; 2005-058069/06.

Depleting B cells from a mixed population of cells by contacting the

cells with a Blys antagonist and a CD20 binding antibody, useful for

treating B cell malignancies and autoimmune disorders.

Disclosure; Fig 8; 114pp; English.

The invention comprises a method of depleting B cells from a mixed

population of cells, the method involves contacting the mixed population

of cells with Blys antagonist (e.g. an immunoadhesin) and a CD20 binding

antibody (e.g. hu2H7.v16). The method of the invention is useful for

treating B cell malignancies and autoimmune disorders, such as: non-

Hodgkin's lymphoma, Hodgkin's disease, follicular center cell lymphomas,

lymphocytic leukemia, hairy cell leukemia, rheumatoid arthritis, systemic

lupus erythematosus, Wegener's disease, inflammatory bowel disease,

idiopathic thrombocytopenic purpura, multiple sclerosis, asthma,

psoriasis, IGA nephropathy, myasthenia gravis, vasculitis, diabetes and

glomerulonephritis. The present amino acid sequence represents a human

TACI protein.

Sequence 266 AA;

Query Match 24.3%; Score 195; DB 9; Length 266;

Best Local Similarity 27.0%; Pred. No. 1.9e-10;

Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

1 MRSCPEQYWAALLGTCMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51

31 MRSCPEQYWDPLGLTGMCKNTICNHQSORTCAAFCSLSCKREQKGFYDHLRLDCISCA 90

52 NACPOS-----TLWPHSQVAEERMAAGDVQ-----76

91 SICQHPKQKAYFCENKLRSPVNLPPELR---RQSGEVENNSDNGRYQGLEHGRSEA 146

77 -----CGTSYPTFLWPHCLLSVSNMPCSSLPVIL-----107

147 SPALPLGLKLSADQVALVYSTGLGLCLVAVACFLKRGDPCSCQPRSRPQSPA 206

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Human lymphocyte surface receptor TACI.

TACI; transmembrane activator and CAML-interactor;

calcium signal-modulating cyclophilin ligand; human;

lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;

cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;

immunosuppressive; graft versus host disease; transplant rejection;

therapy.

Homo sapiens.

Key

Domain

Location/Qualifiers

1. .166

/label= Extracellular\_domain

/note= "Claim 8"

Peptide

34. .71

/note= "TNFR\_NGFR motif"

Domain

167. .186

/label= Transmembrane\_domain

Domain

187. .294

/label= Cytoplasmic\_domain

/note= "Claim 6"

WO9839361-A1.

11-SEP-1998.

03-MAR-1998; 98WO-US004270.

03-MAR-1997; 97US-00810572.

(STUD-) ST JUDE CHILDREN'S RES HOSPITAL.

Bram RJ, Von Bulow G;

WPI; 1998-506346/43.

N-PSDB; AAV57328.

New isolated transmembrane activator protein - used to develop products

for treating e.g. infections, cancers, autoimmune and inflammatory

conditions, transplant rejection or graft-versus-host disease.

Claim 20; Fig 2a; 89pp; English.

This is the amino acid sequence of novel human transmembrane activator

and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is

involved in the calcium activation pathway. TACI is normally present in B

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Human lymphocyte surface receptor TACI.

TACI; transmembrane activator and CAML-interactor;

calcium signal-modulating cyclophilin ligand; human;

lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;

cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;

immunosuppressive; graft versus host disease; transplant rejection;

therapy.

Homo sapiens.

Key

Domain

Location/Qualifiers

1. .166

/label= Extracellular\_domain

/note= "Claim 8"

Peptide

34. .71

/note= "TNFR\_NGFR motif"

Domain

167. .186

/label= Transmembrane\_domain

Domain

187. .294

/label= Cytoplasmic\_domain

/note= "Claim 6"

WO9839361-A1.

11-SEP-1998.

03-MAR-1998; 98WO-US004270.

03-MAR-1997; 97US-00810572.

(STUD-) ST JUDE CHILDREN'S RES HOSPITAL.

Bram RJ, Von Bulow G;

WPI; 1998-506346/43.

N-PSDB; AAV57328.

New isolated transmembrane activator protein - used to develop products

for treating e.g. infections, cancers, autoimmune and inflammatory

conditions, transplant rejection or graft-versus-host disease.

Claim 20; Fig 2a; 89pp; English.

This is the amino acid sequence of novel human transmembrane activator

and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is

involved in the calcium activation pathway. TACI is normally present in B

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KW

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KW

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KW

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KW

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Db 31 MRSCEPQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQVAEERAGGDVQ----- 76  
 Db 91 SICGQHPKQCAYPCEKLRSPVNLPPELR-----RQRSGEVENNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
 Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----FPECRAPTQESAVTP 248

RESULT 11  
 AAB36312  
 ID AAB36312 standard; protein; 293 AA.  
 XX AC AAB36312;  
 XX DT 26-FEB-2001 (first entry)  
 XX DE Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.  
 XX DE Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;  
 KW immunosuppressive; neuroprotic; neuroprotective; antiviral; antiallergic;  
 KW hepatotropic; antidiabetic; antiinflammatory; antiulcer; cardiant;  
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;  
 KW autoimmune disorder.  
 XX OS Homo sapiens.  
 XX PN WO200058362-A1.  
 XX PD 05-OCT-2000.  
 XX PF 24-MAR-2000; 2000WO-US007966.  
 XX PR 26-MAR-1999; 99US-0126599P.  
 XX PR 10-MAR-2000; 2000US-0188208P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Ruben SM, Ullrich S, Baker K;  
 XX WPI; 2000-602359/57.  
 XX N-PSDB; AAC64602.  
 XX Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,  
 PT useful for producing TR17 protein which is used in the treatment and  
 PT diagnosis of autoimmune and immunodeficiency disorders.  
 XX Claim 1; Fig 1; 398pp; English.  
 XX The present sequence represents the human neutrokin-alpha binding (NAR)  
 CC protein designated TR17. TR17 has cytostatic, immunosuppressive,  
 CC neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,  
 CC antidiabetic, antiinflammatory, antiulcer, cardiant and ophthalmological  
 CC activities and can be used in gene therapy. The TR17 protein and  
 CC antibodies are useful for treating and diagnosing immunodeficiency  
 CC disorders and autoimmune disorders. The TR17 polypeptides,  
 CC polynucleotides, antibodies, agonists and/or antagonists are used for  
 CC treating various other diseases defined in the specification and as  
 CC research tools for studying the phenotypic effects that result from  
 CC inhibiting TR17/TR17 ligand interactions on various cell types  
 XX Sequence 293 AA;  
 SQ Query Match 24.3%; Score 195; DB 3; Length 293;  
 Best Local Similarity 27.0%; Pred. No. 2.1e-10;  
 Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

QY 1 MRSCEPQYWAALLGTCTMFCCKAICNHQSORTCAASC-----GEFWDLSFGDSVITP 51  
 Db 31 MRSCEPQYWDPLLGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
 QY 52 NACPQS-----TLWPHSQVAEERAGGDVQ----- 76  
 Db 91 SICGQHPKQCAYPCEKLRSPVNLPPELR-----RQRSGEVENNSDNGRYQGLEHRGSEA 146  
 QY 77 -----CGTSYPSTFLLWPHCLLSVSNMPCSSLPRLV----- 107  
 Db 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRQSPA 206  
 QY 108 -----CTCCSRCLCMLSIIFPOL-PPQLSLGLP 136  
 Db 207 KSSQDHAMEAGSPVSTSPVETCSFC-----FPECRAPTQESAVTP 248

RESULT 12  
 AAY94000  
 ID AAY94000 standard; protein; 293 AA.  
 XX AC AAY94000;  
 XX DT 20-OCT-2000 (first entry)  
 XX DE A transmembrane activator and CAML-interactor (TACI).  
 XX DE Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW ztnf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.  
 XX OS Homo sapiens.  
 XX PN WO2000040716-A2.  
 XX PD 13-JUL-2000.  
 XX PF 07-JAN-2000; 2000WO-US000396.  
 XX PR 07-JAN-1999; 99US-00226533.  
 XX (ZYMO ) ZYMOGENETICS INC.  
 XX Gross JA, Xu W, Madden K, Yee DP;  
 XX WPI; 2000-452538/39.  
 XX N-PSDB; AAA58558.  
 XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.  
 XX Disclosure; Page 149-150; 175pp; English.  
 XX The present sequence represents a human transmembrane activator and CAML-  
 CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)  
 CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI  
 CC or BCMA (a related B cell protein) receptor contain a cysteine rich  
 CC domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF  
 CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA  
 CC receptor-ligand engagement associated with activated or resting B  
 CC lymphocytes, effector T-cells, or with antibody production. The antibody  
 CC production is associated with an autoimmune disease selected from  
 CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and  
 CC rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA



```

PI Goodwin RG, Din WS;
XX WPI; 2001-016005/02.
DR N-PSDB; AAD02006.
XX
XX Use of new interactions between tumor necrosis factor receptors (TACI)
PT and TACI ligands to screen candidate molecules for determining agonist
PT and antagonist interactions which are used for treating inflammation.
XX
XX Claim 10; Fig 1b; 46pp; English.
XX
XX The present sequence is a human tumour necrosis factor receptor (TACI)
CC protein. TACI (Transmembrane activator and calcium-signal modulating
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin
CC alpha polypeptide (TACI-ligand). The antagonist or agonist of TACI/TACI-L
CC complex is useful for modulating an intracellular signalling cascade
CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are
CC used to inhibit the interaction between TACI and TACI-L for therapeutic
CC purposes to treat tumour and tumour metastasis and to combat various
CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as
CC other disorders, such as viral infection, rheumatoid arthritis, graft
CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and
CC inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L acts
CC upon
XX
XX Sequence 293 AA;
XX
XX Query Match 24.3%; Score 195; DB 4; Length 293;
XX Best Local Similarity 27.0%; Pred. No. 2.le-10;
XX Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;
XX
QY 1 MRSCPEQYWAALGTGTCMFKATCNHQSORTCAASC-----GEFWDLSFGDSVITP 51
DQ ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
DQ 31 MRSCPEQYWDPLLTGTCMCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90
QY 52 NACPQS-----TLWPHSQVAERMGAGDVQ----- 76
DQ : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
DQ 91 SIGGHPKQCAFCENKLRSPVNLPELR-----RQRSGEVNNSDNGRYQGLEHRGSEA 146
QY 77 -----CGTSYSPSTFLWPHCLLSVSNMPCSSLPVYL----- 107
DQ ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY 108 -----CTCCSRCLCMLSIIPQL-PPTQLSGLGP 136
DQ 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----FPCEAPQESAVTP 248
XX
RESULT 15
AAO14130
XX ID AAO14130 standard; protein; 293 AA.
XX
XX AAO14130;
XX
XX 02-MAY-2002 (first entry)
XX
XX Human transmembrane activator CAML interactor protein (TACI).
XX
XX Human transmembrane activator CAML interactor protein; TACI; cytostatic;
KW cell proliferation; tumour; vulvar; renal cell cancer; mastocytoma;
KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;
KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;
KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;
KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;
KW uterine.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers

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Search completed: December 20, 2005, 10:38:53  
Job time : 188 secs

| Result No. | Score | Query |     | Length | DB                 | ID | Description       |
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| 1          | 803   | 100.0 | 142 | 4      | US-09-618-797-2    |    | Sequence 2, Appli |
| 2          | 198.5 | 24.7  | 291 | 3      | US-09-779-050A-43  |    | Sequence 43, Appl |
| 3          | 198   | 24.7  | 293 | 3      | US-09-779-050A-42  |    | Sequence 42, Appl |
| 4          | 195   | 24.3  | 265 | 5      | US-10-626-914-17   |    | Sequence 17, Appl |
| 5          | 195   | 24.3  | 265 | 5      | US-10-626-914-17   |    | Sequence 19, Appl |
| 6          | 195   | 24.3  | 265 | 5      | US-10-861-049-36   |    | Sequence 36, Appl |
| 7          | 195   | 24.3  | 265 | 6      | US-11-021-874-36   |    | Sequence 36, Appl |
| 8          | 195   | 24.3  | 293 | 3      | US-09-879-919-22   |    | Sequence 22, Appl |
| 9          | 195   | 24.3  | 293 | 3      | US-09-854-864-14   |    | Sequence 14, Appl |
| 10         | 195   | 24.3  | 293 | 3      | US-09-855-158-14   |    | Sequence 14, Appl |
| 11         | 195   | 24.3  | 293 | 3      | US-09-961-376-2    |    | Sequence 2, Appli |
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| 13         | 195   | 24.3  | 293 | 4      | US-09-855-564-2    |    | Sequence 2, Appli |
| 14         | 195   | 24.3  | 293 | 4      | US-10-087-192-1650 |    | Sequence 1650, Ap |
| 15         | 195   | 24.3  | 293 | 4      | US-10-084-971-2    |    | Sequence 2, Appli |
| 16         | 195   | 24.3  | 293 | 4      | US-10-068-725-4    |    | Sequence 4, Appli |
| 17         | 195   | 24.3  | 293 | 4      | US-10-151-882-46   |    | Sequence 46, Appl |
| 18         | 195   | 24.3  | 293 | 4      | US-10-293-816-2    |    | Sequence 2, Appli |
| 19         | 195   | 24.3  | 293 | 4      | US-10-008-063-8    |    | Sequence 8, Appli |
| 20         | 195   | 24.3  | 293 | 4      | US-10-152-363A-2   |    | Sequence 2, Appli |
| 21         | 195   | 24.3  | 293 | 4      | US-10-268-951-22   |    | Sequence 22, Appl |
| 22         | 195   | 24.3  | 293 | 4      | US-10-258-368-1    |    | Sequence 1, Appli |
| 23         | 195   | 24.3  | 293 | 4      | US-10-618-797-4    |    | Sequence 4, Appli |
| 24         | 195   | 24.3  | 293 | 4      | US-10-742-634-7    |    | Sequence 7, Appli |
| 25         | 195   | 24.3  | 293 | 4      | US-10-748-113-27   |    | Sequence 27, Appl |
| 26         | 195   | 24.3  | 293 | 5      | US-10-684-149-4    |    | Sequence 4, Appli |
| 27         | 195   | 24.3  | 293 | 5      | US-10-626-914-3    |    | Sequence 3, Appli |

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; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-43

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Best Local Similarity 27.0%; Pred. No. 7.9e-11;
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QY      52 NACPQS-----TLWPHSOVAERMAAGDVQ-----76
Db      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQSGEVENNSDNGRYQGLEHRGSEA 146
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
Db      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCCFLVAVACFLKMRGDPCCSQPRSRPRQSPA 206
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
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RESULT 3
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; Sequence 42, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-779-050A-42

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QY      1 MRSCPEQYWAALGTCMFCCKAICNHQSORTCAASC-----GEFWDLSPGDSVITP 51
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QY      52 NACPQS-----TLWPHSOVAERMAAGDVQ-----76
Db      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQSGEVENNSDNGRYQGLEHRGSEA 146
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
Db      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCCFLVAVACFLKMRGDPCCSQPRSRPRQSPA 206
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
Db      207 KSSQDHAMEAGSPVSTSPPEVETCSFC-----PFECRAPTQESAVTP 248

RESULT 4
US-10-626-914-17
; Sequence 17, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, IOBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-626-914-17

Query Match      24.3%; Score 195; DB 5; Length 265;
Best Local Similarity 27.0%; Pred. No. 1.5e-10;
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

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QY      52 NACPQS-----TLWPHSOVAERMAAGDVQ-----76
Db      91 SICGQHPKQCAFCENKLRSPVNLPELR-----RQSGEVENNSDNGRYQGLEHRGSEA 146
QY      77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPRLV-----107
Db      147 SPALPGLKLSADQVAVYSTLGLCLCAVLCCFLVAVACFLKMRGDPCCSQPRSRPRQSPA 206
QY      108 -----CTCCSRCLCMLSIIFPOL-PPTQLSLGLP 136
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RESULT 5
US-10-485-489-19
; Sequence 19, Application US/10485489
; Publication No. US20050070689A1
; GENERAL INFORMATION:
; APPLICANT: Dixit, Vishva
; APPLICANT: Grewal, Iqbal
; APPLICANT: Ridgway, John
; APPLICANT: Yan, Minhong
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof
; FILE REFERENCE: 11669.175USWO
; CURRENT APPLICATION NUMBER: US/10/485,489
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/US02/23487
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/310,114
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/377,171
; PRIOR FILING DATE: 2002-04-30
; NUMBER OF SEQ ID NOS: 19
; SEQ ID NO 19
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-489-19

Query Match      24.3%; Score 195; DB 5; Length 265;
Best Local Similarity 27.0%; Pred. No. 1.5e-10;
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Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
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Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ-----76  
Db 91 SICQHPKQCAFCENKLRSPVNLPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV-----107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
Qy 108 -----CTCCSRCLCMLSIIFFPOL-PPTOLSLGLP 136  
Db 207 KSSQDHAMEAGSPVSTSPPEVETCSFC-----FPECRAPTQESAVTP 248

RESULT 6  
US-10-861-049-36  
; Sequence 36, Application US/10861049  
; Publication No. US20050095243A1  
; GENERAL INFORMATION:  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R101US  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-049-36

Query Match 24.3%; Score 195; DB 5; Length 265;  
Best Local Similarity 27.0%; Pred. No. 1.5e-10;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;  
Qy 1 MRSCPEQYWAALIGTCMFCCKAICNHOSQRTCAASC-----GEFWDLSPGDSVITP 51  
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Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ-----76  
Db 91 SICQHPKQCAFCENKLRSPVNLPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV-----107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
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RESULT 7  
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; Sequence 36, Application US/11021874  
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; GENERAL INFORMATION:  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; APPLICANT: Qian Gong  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R101US  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-36

; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R101  
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; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
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; ORGANISM: Homo sapiens  
US-11-021-874-36

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Qy 52 NACPQS-----TLWPHSQVAEREMAGDVQ-----76  
Db 91 SICQHPKQCAFCENKLRSPVNLPELR-----RQRSEVENNSDNGRYQGLEHGRSEA 146  
Qy 77 -----CGTSPSTFLLWPHCLLSVSNMPCSSLPRLV-----107  
Db 147 SPALPGLKLSADQVALVYSTLGLCLCAVLCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
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RESULT 8  
US-09-879-919-22  
; Sequence 22, Application US/09879919  
; Patent No. US20020064829A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: PF253PI  
; CURRENT APPLICATION NUMBER: US/09/879,919  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254,875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241,952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211,537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815,783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016,812  
; PRIOR FILING DATE: 1996-03-14  
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; SOFTWARE: PatentIn Ver. 2.1  
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; ORGANISM: Homo sapiens  
US-09-879-919-22



Query Match 24.3%; Score 195; DB 3; Length 293;  
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QY 77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPVRL----- 107  
DB 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
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RESULT 12  
US-09-302-863-2  
; Sequence 2, Application US/09302863  
; Publication No. US2003002233A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G  
; APPLICANT: Din, Wanwan S.  
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION  
; FILE REFERENCE: 2519  
; CURRENT APPLICATION NUMBER: US/09/302,863  
; CURRENT FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Human  
US-09-302-863-2

Query Match 24.3%; Score 195; DB 3; Length 293;  
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DB 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
DB 91 SICGHPKQKQAYFCENKLRSPVNLPPELR-----RQSRGEVNNDSNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPVRL----- 107  
DB 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
QY 108 -----CTCCSRCLCMLSIIPPOL-PPTQLSLGLP 136  
DB 207 KSSQDHAMEAGSPVSTSPPEVETCSFC-----FPECRAPTQESAVTP 248

RESULT 13  
US-09-855-564-2  
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; Publication No. US20030165986A1  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G  
; APPLICANT: Din, Wanwan S.  
; TITLE OF INVENTION: METHODS OF USE OF THE TACI/TACI-L INTERACTION  
; FILE REFERENCE: 2519  
; CURRENT APPLICATION NUMBER: US/09/855,564  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 09/302,863  
; PRIOR FILING DATE: 1999-04-30  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
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; TYPE: PRT  
; ORGANISM: Human  
US-09-855-564-2

Query Match 24.3%; Score 195; DB 3; Length 293;  
Best Local Similarity 27.0%; Pred. No. 1.7e-10;  
Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

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DB 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
DB 91 SICGHPKQKQAYFCENKLRSPVNLPPELR-----RQSRGEVNNDSNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPVRL----- 107  
DB 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
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RESULT 14  
US-10-087-192-1650  
; Sequence 1650, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1650  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-087-192-1650

Query Match 24.3%; Score 195; DB 4; Length 293;  
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Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

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DB 31 MRSCPEQYWDPLLTGTCMSCKTICNHQSORTCAAFCSRSLSCRKEQKGFYDHLRLDCISCA 90  
QY 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76  
DB 91 SICGHPKQKQAYFCENKLRSPVNLPPELR-----RQSRGEVNNDSNGRYQGLEHGRSEA 146  
QY 77 -----CGTSYPSTFLWPHCLLSVSNMPCSSLPVRL----- 107  
DB 147 SPALPGLKLSADQVALVYSTGLCLCAVLCCFLVAVACFLKRGDPCSCQPRSRPROSPA 206  
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RESULT 15  
US-10-084-971-2  
; Sequence 2, Application US/10084971  
; Publication No. US20020187526A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:34 ; Search time 228 Seconds  
(without alignments)  
439.408 Million cell updates/sec

Title: US-10-618-797-2

Perfect score: 803

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description  |
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| 2          | 195   | 24.3        | 293    | 1     | Q14836 HUMAN |
| 3          | 107.5 | 13.4        | 140    | 2     | Q5U833 MOUSE |
| 4          | 107.5 | 13.4        | 249    | 1     | Q14836 HUMAN |
| 5          | 107.5 | 13.4        | 249    | 2     | Q5U833 MOUSE |
| 6          | 99    | 12.3        | 704    | 2     | Q74567 TRIHA |
| 7          | 98    | 12.2        | 1299   | 2     | Q26489 SPOPR |
| 8          | 97    | 12.1        | 949    | 2     | Q5DNW1 TRINI |
| 9          | 96    | 12.0        | 74     | 2     | Q5U844 MOUSE |
| 10         | 95    | 11.8        | 300    | 1     | TNR6B HUMAN  |
| 11         | 94    | 11.7        | 459    | 2     | Q62327 MOUSE |
| 12         | 94    | 11.7        | 474    | 1     | TNR1B MOUSE  |
| 13         | 94    | 11.7        | 474    | 2     | Q545P4 MOUSE |
| 14         | 93    | 11.6        | 5141   | 2     | Q700K0 RAT   |
| 15         | 90    | 11.2        | 286    | 2     | Q8AXC0 XENLA |
| 16         | 89    | 11.1        | 1656   | 2     | Q50S87 ENTHI |
| 17         | 88.5  | 11.0        | 251    | 2     | Q919W2 SCALL |
| 18         | 88.5  | 11.0        | 862    | 2     | Q8K0T1 MOUSE |
| 19         | 88.5  | 11.0        | 1223   | 2     | Q68PF6 MOUSE |
| 20         | 88.5  | 11.0        | 1262   | 2     | Q80T73 MOUSE |
| 21         | 88.5  | 11.0        | 1675   | 2     | Q9VLT1 DROME |
| 22         | 88    | 11.0        | 4010   | 1     | FRAS1 MOUSE  |
| 23         | 87.5  | 10.9        | 4998   | 2     | Q8CG65 MOUSE |
| 24         | 87.5  | 10.9        | 724    | 2     | Q4ZJ75 XENLA |
| 25         | 87.5  | 10.9        | 729    | 2     | Q6GPT6 XENLA |
| 26         | 87    | 10.8        | 1083   | 2     | Q51CE3 ENTHI |
| 27         | 86.5  | 10.8        | 235    | 2     | Q91YP4 MOUSE |
| 28         | 86.5  | 10.8        | 1036   | 2     | Q80T21 MOUSE |
| 29         | 86    | 10.7        | 277    | 2     | Q5T8X4 HUMAN |
| 30         | 85    | 10.6        | 557    | 2     | Q4R7B7 MACPA |
| 31         | 85    | 10.6        | 589    | 1     | GRN_MOUSE    |

|    |      |      |      |   |              |
|----|------|------|------|---|--------------|
| 32 | 85   | 10.6 | 589  | 2 | Q544Y8 MOUSE |
| 33 | 85   | 10.6 | 602  | 2 | Q9D2V3 MOUSE |
| 34 | 85   | 10.6 | 1642 | 2 | Q515F7 ENTHI |
| 35 | 84.5 | 10.5 | 596  | 2 | Q51ZD5 MAGGR |
| 36 | 84.5 | 10.5 | 1030 | 2 | Q4FZU4 RAT   |
| 37 | 84.5 | 10.5 | 1061 | 2 | Q5B110 DROME |
| 38 | 84.5 | 10.5 | 1679 | 1 | FUR2 DROME   |
| 39 | 84   | 10.5 | 465  | 2 | Q7QVC3 GIALA |
| 40 | 83.5 | 10.4 | 433  | 2 | Q91ZM6 RAT   |
| 41 | 83.5 | 10.4 | 461  | 2 | Q6VAU8 RAT   |
| 42 | 83.5 | 10.4 | 474  | 1 | TNR1B RAT    |
| 43 | 83.5 | 10.4 | 474  | 2 | Q5YLP0 RAT   |
| 44 | 83.5 | 10.4 | 1877 | 1 | PCSK5 MOUSE  |
| 45 | 82.5 | 10.3 | 251  | 2 | Q919X6 CENUR |

## ALIGNMENTS

### RESULT 1

Q53F36\_HUMAN  
ID Q53F36 HUMAN PRELIMINARY; PRT; 293 AA.  
AC Q53F36;  
DT 13-SEP-2005 (Tremblrel. 31, Created)  
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)  
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)  
DE Tumor necrosis factor receptor 13B variant (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Small intestine;  
RA Maruyama K., Sugano S.;  
RT "Oligo-capping: a simple method to replace the cap structure of eucaryotic mRNAs with oligoribonucleotides";  
RL Gene 138171-174 (1994).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Small intestine;  
RA Suzuki Y., Yoshitomo K., Maruyama K., Sugano A., Sugano S.;  
RT "Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library.";  
RL Gene 200149-156 (1997).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Small intestine;  
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.;  
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK223453; BAD97173.1; -; mRNA.  
FT NON TER.  
SQ SEQUENCE 293 AA; 31846 MW; D9EA2F28B3BF466D CRC64;

Query Match 24.4%; Score 196; DB 2; Length 293;

Best Local Similarity 27.0%; Pred. No. 1.1e-10;

Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;

Qy 1 MRSCPBYQYWAALIGTCMFCATCNHOSQRTCAASC-----GEFWDLSPGDSVITP 51

Db 31 MRSCPBYQYWDPLGLTGMSCKTICNHOSQRTCAAFCSLRSCKRQKGFYDHLRLDCTSCA 90

Qy 52 NACPQS-----TLPHSQVAERMAAGDVQ----- 76

Db 91 SICGHPKQCAFCENKLRSPVNLPELR---RQRSGEVENNSDNGRYQGLEHRSSEA 146

Qy 77 -----CGTSPSTFLWPHCLLSVSNMPCSSLPRVL----- 107

Db 147 SPALPLGLKSADQVALVYTLGLCLCAVLCAEACFLKRGDPCSCQPRSPROSPA 206

Qy 108 -----CTCSRCLCMLSIIFPQL-PPTQLSLGLP 136

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Db      207 KSSQDHAMEAGSPVTSPEVETCSFC-----PFECRAPTOESAVTP 248
RESULT 2
TR13B HUMAN STANDARD; PRT; 293 AA.
AC O14836; Q726F5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Names=TNFRSF13B; Synonyms=TACI;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 1).
RC TISSUE=B-cell;
RX MEDLINE=97456245; PubMed=93111921; DOI=10.1126/science.278.5335.138;
RA von Buelow G.-U., Bram R.J.;
RT "NF-AT activation induced by a CAML-interacting member of the tumor
RT necrosis factor receptor superfamily.";
RL Science 278:138-141(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE (MRNA) (ISOFORM 2).
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinko D., Lafleur D.,
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
RA Olson H.S., Kanakaraj P., Moore P.A., Baker K.P.;
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a
RT high affinity receptor for TNF family members APRIL and BlyS.";
RL J. Biol. Chem. 275:35478-35485(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Scollina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theilli L.E.,
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity.";
RL Nat. Immunol. 1:252-256(2000).
RN [5]
RP INTERACTIONS WITH TRAF2 AND TRAF3.
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theilli L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Scollina M., Yu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.;
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 68-109, AND STRUCTURE BY NMR
RP OF 68-109.
RX PubMed=15542592; DOI=10.1074/jbc.M411714200;
RA Hymowitz S.G., Patel D.R., Wallweber H.J., Runyon S., Yan M., Yin J.,
RA Shriver S.K., Gordon N.C., Pan B., Skelton N.J., Kelley R.F.,
RA Starovasnik M.A.;
RT "Structures of APRIL-receptor complexes: like BCMA, TACI employs only
RT a single cysteine-rich domain for high affinity ligand binding.";
RL J. Biol. Chem. 280:7218-7227(2005).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation

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CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity.
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus.
CC -1- INTERACTION:
CC O75888:TNFSF13; NExp=1; IntAct=EBI-519160, EBI-519208;
CC Q9Y275:TNFSF13B; NExp=4; IntAct=EBI-519160, EBI-519169;
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O14836-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O14836-2; Sequence=VSP_013798;
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
CC intestine and peripheral blood leukocytes. Expressed in resting B-
CC cells and activated T-cells, but not in resting T-cells.
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF023614; AAC51790.1; -; mRNA.
CC EMBL; AY302137; AAP57629.1; -; mRNA.
CC PDB; 1XU1; X-ray; R/S/T=68-109.
CC PDB; 1XUT; NMR; A=68-109.
CC IntAct; O14836; -.
CC Ensembl; ENSG00000108516; Homo sapiens.
CC HGNC; HGNC:18153; TNFRSF13B.
CC MIM; 604907; -.
CC GO; GO:0005887; C-integral to plasma membrane; TAS.
CC GO; GO:0004872; P-receptor activity; TAS.
CC GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
CC InterPro; IPR001368; TNFR_C6.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
CC 3D-structure; Alternative splicing; Glycoprotein; Immune response;
CC Receptor; Repeat; Signal-anchor; Transmembrane.
CC TOPO_DOM 1 165 Extracellular (Potential).
CC TRANSMEM 166 186 Signal-anchor for type III membrane
CC protein (Potential).
CC REPEAT 33 67 Cytoplasmic (Potential).
CC REPEAT 70 104 TNFR-Cys 1.
CC CARBOHYD 128 128 N-linked (GlcNAc...) (Potential).
CC DISULFID 34 47 By similarity.
CC DISULFID 50 62 By similarity.
CC DISULFID 54 66 By similarity.
CC DISULFID 71 86
CC DISULFID 89 100
CC DISULFID 93 104
CC VARSPLIC 21 67
CC
CC SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
CC
CC Query Match 24.3%; Score 195; DB 1; Length 293;
CC Best Local Similarity 27.0%; Pred. No. 1.4e-10;
CC Matches 62; Conservative 11; Mismatches 51; Indels 106; Gaps 7;
CC
CC QY 1 MRSCPQYWAALIGTCMFKCAICNHQSORTCAASC-----GFWDLSPGDSVITP 51
CC DB 31 MRSCPQYWDPLLTGCTMCKTICNHQSORTCAAFCSLSCKRQKGFYDHLRLDCISCA 90
CC QY 52 NACPQS-----TLWPHSQVAERMAAGDVQ----- 76
CC DB 91 SICGQHPKQCAFCNCKLRSPVNLPPELR-----QRSGEVENNSDNGRYQGLEHRSSEA 146
CC QY 77 -----CGTSYPSFTLLWPHCLLSVSNMPCSSLPRLV----- 107

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Db 147 SPALPGLKLSADQVALVYVTLGLCLVACFLKRGKRGPCQSPRSPQSPA 206
Qy 108 -----CTCSRCRLCMLSIIPQL-PPTQLSLGP 136
Db 207 KSSQDHAMEAGSPVSTSPVPVETCSFC-----PPECRAPTOSSAVTP 248

RESULT 3
Q55U83_MOUSE
ID Q55U83_MOUSE PRELIMINARY; PRT; 140 AA.
AC Q55U83;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b
DE (Fragment).
GN Name=Tnfrsf13b; ORFNames=RP23-5512.2-003;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Holt K.;
RL Submitted (PEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CA125895.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 140
SQ SEQUENCE 140 AA; 15672 MW; 005D8CDF4E8B3D15 CRC64;

Query Match 13.4%; Score 107.5; DB 2; Length 140;
Best Local Similarity 32.3%; Pred. No. 0.018;
Matches 21; Conservative 10; Mismatches 25; Indels 9; Gaps 1;

Qy 1 MRSCPQYQVWALGTCMFCAICNHSQRTCAASC-----GFWDLSQDGVITP 51
Db 3 MAPCPQYQVWDSRKSVCVSCALTCQSRSQRTCTDFCKFNCRKQGRYYDHLGACVSCD 62

Qy 52 NACPQ 56
Db 63 STCTQ 67

RESULT 4
TR13B_MOUSE
ID TR13B_MOUSE STANDARD; PRT; 249 AA.
AC Q9ET35; Q9DBZ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
DE activator and CAML interactor).
GN Name=Tnfrsf13b; Synonyms=taci;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Spleen;
RX MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
RY Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
RT "Identification of a receptor for Blys demonstrates a crucial role in
RT humoral immunity.";
RL Nat. Immunol. 1:37-41(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

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RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirani L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
RA Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RN [3]
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP FUNCTION.
RX MEDLINE=20341628; PubMed=10880535; DOI=10.1084/jem.192.1.137;
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
RA Theilli L.E., Colombero A., Solovyeve I., Lee P., McCabe S., Elliott R.,
RA Miner K., Hawkins N., Guo J., Stolina M., Fu G., Wang J., Delaney J.,
RA Meng S.-Y., Boyle W.J., Hsu H.;
RT "TAC1 is a TRAF-interacting receptor for TALL-1, a tumor necrosis
RT factor family member involved in B cell regulation.";
RL J. Exp. Med. 192:137-143(2000).
RN [4]
RP FUNCTION.
RX MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;
RA Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
RA Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT "TAC1-ligand interactions are required for T cell activation and
RT collagen-induced arthritis in mice.";
RL Nat. Immunol. 2:632-637(2001).
CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BALF/BLYS
CC that binds both ligands with similar high affinity. Mediates
CC calcineurin-dependent activation of NF-AT, as well as activation
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC cell function and the regulation of humoral immunity (By
CC similarity).
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC domain of CAMLG with its C-terminus (By similarity).
CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; AF257673; AAC00081.1; -; mRNA.
CC EMBL; AK004668; BAB23457.1; -; mRNA.
CC EMBL; ENSMUSG0000010142; Mus musculus.
CC MGI; MGI:1899411; Tnfrsf13b.
CC GO; GO:0009897; C:external side of plasma membrane; IDA.
CC GO; GO:0005887; C:integral to plasma membrane; IDA.
CC GO; GO:0001782; P:B cell homeostasis; IMP.
CC GO; GO:0030889; P:negative regulation of B cell proliferation; IMP.
CC InterPro; IPR001368; TNFR c6.
CC PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.

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|                  |   |
|------------------|---|
| GN               | Name=qid74;   |
| OS               | Trichoderma harzianum (Hypocrea lixii).                                 |
| OC               | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;          |
| OC               | Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.                 |
| NCBI_TaxID=5544; |   |
| OX               | [1]   |
| RN               | Nucleotide sequence.  |
| RP               | STRAIN=CECT 2413;   |
| RC               | MEDLINE=98463335; PubMed=9600944; DOI=10.1073/pnas.95.11.6212;          |
| RA               | Key M., Ohno S.A., Pintor-Toro J.A., Jose A., Liebell A., Benitez T.;   |
| RT               | "Unexpected homology between inducible cell wall protein of             |
| RT               | filamentous fungi and BR3 salivary protein of the insect Chironomus.";  |
| RL               | Proc. Natl. Acad. Sci. U.S.A. 95:6212-6216(1998).                       |
| DR               | EMBL; X95671; CAA64974.1; -; mRNA.                                      |
| DR               | GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.            |
| DR               | GO; GO:0005509; F:calcium ion binding; IEA.                             |
| DR               | GO; GO:0004872; F:receptor activity; IEA.                               |
| DR               | GO; GO:0007275; P:development; IEA.                                     |
| DR               | GO; GO:0007399; P:neurogenesis; IEA.                                    |
| DR               | InterPro; IPR006209; EGF like.  |
| DR               | PROSITE; PS01186; EGF_2; 1.   |
| KW               | Repeat.   |
| SQ               | SEQUENCE 704 AA; 77925 MW; 63414BDDDEC365EBC CRC64;                     |
|                  |   |
|                  | Query Match 12.3%; Score 99; DB 2; Length 704;                          |
|                  | Blast Local Similarity 22.1%; Pred. No. 0.63;                           |
|                  | Matches 32; Conservative 14; Mismatches 37; Indels 62; Gaps 8;          |
| QY               | 3 SPDEEYWAALIGTCMF-----C-----KACNHQSQ-----RTCA 33                       |
| DB               | 508 SCFDSYGSGSKCACPYGTWDGKHCHQCQDKAHFDNSNQKCKVQGEVDYSKTKCS 567          |
| QY               | 34 ASGGEFWLSPGDVSITPACPOSTLPHSQVAERAMAGDVGCG--TSVPSTFLLPHC 91           |
| DB               | 568 CPDGQWDGS-----KCACYGVKWDGKQCV-----NCGKDASYDS-----604                |
| QY               | 92 LLSGVNMPCSSLPVL-----CTC 110  |
| DB               | 605 --KQNKVCVKNIQQVDTKSLTCS 627   |
| RESULT 7         |   |
| Q26489_SPOFR     | PRELIMINARY; PRT; 1299 AA.  |
| ID               | Q26489_SPOFR PRELIMINARY; PRT; 1299 AA.                                 |
| AC               | Q26489;   |
| DT               | 01-NOV-1996 (TEMBLrel. 01, Created)                                     |
| DT               | 01-NOV-1996 (TEMBLrel. 01, Last sequence update)                        |
| DT               | 01-MAR-2004 (TEMBLrel. 26, Last annotation update)                      |
| DE               | Endoprotease FUJIN.   |
| GN               | Name=FUJIN;   |
| OS               | Spodoptera frugiperda (Fall armyworm).                                  |
| OC               | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;           |
| OC               | Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;   |
| OC               | Noctuidae; Amphipyrinae; Spodoptera.                                    |
| NCBI_TaxID=7108; |   |
| OX               | [1]   |
| RN               | Nucleotide sequence.  |
| RP               | TISSUE=Sf9;   |
| RC               | Cieplik M., Klenk H.;   |
| RA               | Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.                |
| RL               | EMBL; Z68888; CAA93116.1; -; mRNA.                                      |
| DR               | PIR; T43251; T43251.  |
| DR               | HSSP; P23188; IP8J.   |
| DR               | GO; GO:0016020; C:membrane; IEA.  |
| DR               | GO; GO:0005524; F:ATP binding; IEA.                                     |
| DR               | GO; GO:0006233; F:peptidase activity; IEA.                              |
| DR               | GO; GO:0004289; F:subtilase activity; IEA.                              |
| DR               | GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . ; IEA. |
| DR               | GO; GO:0006468; P:protein amino acid phosphorylation; IEA.              |
| DR               | GO; GO:0005508; P:proteolysis and peptidolysis; IEA.                    |
| DR               | GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA. |
| DR               | InterPro; IPR006212; Furin repeat.                                      |
| DR               | InterPro; IPR000209; Pept_S8_SF3.                                       |



```
DR InterPro; IPR002884; P:protnconvertap.
DR Pfam; PF01483; P:proteolysin; 1.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR SMART; SM00261; FU; 10.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 1299 AA; 142020 MW; 4C3799C7B5C572AB CRC64;

Query Match 12.2%; Score 98; DB 2; Length 1299;
Best Local Similarity 25.9%; Pred. No. 1.5;
Matches 36; Conservative 15; Mismatches 58; Indels 30; Gaps 7;

Qy 1 MRSCPEQYWAALLGTCMFCVKAICNHOSQRT--CAASCGEFWDLSPGDSVITPACPOSTL 58
Db 781 LQQCPDGYDESSVCRPAAHCAATCSERADGC-TSCHEHLVLHDGTCLMA---SCPPS- 835
Qy 59 LWPHSQVAERMA-----GGDVQCGTSYSPFTLLWPHCLLSV-----SNMP 99
Db 836 ---HYETEDMCAKCHESCDTCQSGRAQCVTCHPSTVALDGRCTVCPAYYADKKRKE 892
Qy 100 CSSLPRLVLTCCSR-CLEC 117
Db 893 CMRCFVGCSTCTSAFCLSC 911

RESULT 8
QSDNW1 TRINI PRELIMINARY; PRT; 949 AA.
AC QSDNW1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Furin-like convertase.
OS Trichoplusia ni (Cabbage looper).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Plusiinae; Trichoplusia.
OX NCBI_TaxID=7111;
RN [1]
RA Wang L., Yang G., Wu X.;
RT "Cloning, expression, and characterization of recombinant Tn5 cells
RT furin-like convertase from baculovirus-infected insect cells.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY555267; AAT37510.1; -; mRNA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004289; F:subtilase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR002884; P:protnconvertap.
DR Pfam; PF01483; P:proteolysin; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PRODOM; PD000717; P:protnconvertap; 1.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
SQ SEQUENCE 949 AA; 104439 MW; 32C4731E491F968C CRC64;

Query Match 12.1%; Score 97; DB 2; Length 949;
Best Local Similarity 25.9%; Pred. No. 1.3;
Matches 36; Conservative 13; Mismatches 60; Indels 30; Gaps 7;

Qy 1 MRSCPEQYWAALLGTCMFCVKAICNHOSQRT--CAASCGEFWDLSPGDSVITPACPOSTL 59
Db 781 LQQCPDGYDESSVCRPAAHCAATCSERADGC-TSCHEHLVLHDGTCLMA---SCPPS- 835
Qy 60 WPHSQVAERMA-----GGDVQCGTSYSPFTLLWPHCLLSV-----SNMPC 100

Db 836 --HYETEDMCAKCHESCDTCGSGRAQCVTCHPSTVALDGRCTVCPAYYADKKRKE 893
Qy 101 SSLPRLVLTCCSR--CLEC 117
Db 894 MRCP-VGCASCTSAFCLSC 911

RESULT 9
QSSU84 MOUSE PRELIMINARY; PRT; 74 AA.
AC QSSU84;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 13b
DE (Fragment).
GN Names=TNFRsf13b; ORFNames=RP23-55I2.2-002;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Holt K.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL646093; CAI25894.1; -; Genomic DNA.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 74
SQ SEQUENCE 74 AA; 8337 MW; DA8A3B06FE191A26 CRC64;

Query Match 12.0%; Score 96; DB 2; Length 74;
Best Local Similarity 41.7%; Pred. No. 0.12;
Matches 15; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MRSCPEQYWAALLGTCMFCVKAICNHOSQRTCAASC 36
Db 3 MAFCPDQYWDSSKSCVSCALTCQSQRSTCTDPC 38

RESULT 10
TNR6B HUMAN STANDARD; PRT; 300 AA.
AC OS5407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
DE receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).
GN Name=TNFRSF6B; Synonyms=DCR3, TR6; ORFNames=UNQ186/PRO212;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703 (1998).
RN [2]
RA NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=10318773; DOI=10.1074/jbc.274.20.13733;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
```

RT "A newly identified member of tumor necrosis factor receptor  
 RT superfamily (TRF) suppresses LIGHT-mediated apoptosis.";  
 RL J. Biol. Chem. 274:13733-13736(1999).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Lung;  
 RX MEDLINE=20122600; PubMed=10655513; DOI=10.1073/pnas.97.3.1230;  
 RA Bai C., Connolly B., Metzger M.L., Hilliard C.A., Liu X., Sandig V.,  
 RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;  
 RT "Overexpression of M68/Dc33 in human gastrointestinal tract tumors  
 RT independent of gene amplification and its location in a four-gene  
 RT cluster.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).  
 RL [4]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,  
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,  
 RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
 RA Vandlen R.L., Watanabe C., Weand D., Woods K., Xie M.-H., Goddard A.D.,  
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,  
 RA Wood W.I., Godowski P.J., Gray A.M.;  
 RT "The secreted protein discovery initiative (SPDI), a large-scale  
 RT effort to identify novel human secreted and transmembrane proteins: a  
 RT bioinformatics assessment.";  
 RL Genome Res. 13:2265-2270(2003).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;  
 RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grafham D.V., Griffiths M.N.D., Griffiths J.L., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Lehesvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,  
 RA Milne S.A., Mistry S., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,  
 RA Stuke C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 RN [6]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC TISSUE=Lung, and Skin;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lomelianno N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT  
 CC and TNFSF6/FASL. Protects against apoptosis.  
 CC -1- INTERACTION:  
 CC O43557:TNFSF14; NDEP=1; IntAct=EBI-524171, EBI-524131;  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.  
 CC Detected in adult stomach, spinal cord, lymph node, trachea,  
 CC spleen, colon and lung. Highly expressed in several primary tumors  
 CC from colon, stomach, rectum, esophagus and in SW480 colon  
 CC carcinoma cells.  
 CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.  
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 DR ENBL; AF104419; AAD03056.1; -; mRNA.  
 DR ENBL; AF134240; AAD29688.1; -; mRNA.  
 DR ENBL; AF217796; AAF35244.1; -; Genomic\_DNA.  
 DR ENBL; AF217793; AAF33685.1; -; mRNA.  
 DR ENBL; AF217794; AAF33686.1; -; mRNA.  
 DR ENBL; AV358279; AAQ8646.1; -; mRNA.  
 DR ENBL; AL121845; CAC03668.1; -; Genomic\_DNA.  
 DR ENBL; BC017065; AAH17065.1; -; mRNA.  
 DR ENBL; BC034349; AAH34349.1; -; mRNA.  
 DR HSSP; O14763; 1DU3.  
 DR Ensembl; O95407; -;  
 DR Ensembl; ENSG0000026036; Homo sapiens.  
 DR HGNC; HGNC:11921; TNFRSF6B.  
 DR H-InvDB; HIX0016007; -;  
 DR MIM; 603361; -;  
 DR GO; GO:0005625; C:soluble fraction; TAS.  
 DR GO; GO:0004872; F:receptor activity; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 2.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat;  
 KW Signal.  
 FT SIGNAL  
 FT CHAIN 1 29 Tumor necrosis factor receptor  
 FT CHAIN 30 30 superfamily member 6B.  
 FT REPEAT 31 70 TNFR-Cys 1.  
 FT REPEAT 72 113 TNFR-Cys 2.  
 FT REPEAT 115 150 TNFR-Cys 3.  
 FT REPEAT 152 193 TNFR-Cys 4.  
 FT REPEAT 173 173 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 49 62 By similarity.  
 FT DISULFID 52 70 By similarity.  
 FT DISULFID 73 88 By similarity.  
 FT DISULFID 91 105 By similarity.  
 FT DISULFID 95 113 By similarity.  
 FT DISULFID 115 126 By similarity.  
 FT DISULFID 132 150 By similarity.  
 FT DISULFID 152 168 By similarity.  
 FT DISULFID 174 193 By similarity.  
 SQ SEQUENCE 300 AA; 32680 MW; F90AE33718449AF CRC64;  
 Query Match 11.8%; Score 95; DB 1; Length 300;

```

Best Local Similarity 25.2%; Pred. No. 0.63;
Matches 36; Conservative 9; Mismatches 46; Indels 52; Gaps 7;

Qy 4 CPBE---QYWAALGTCHFKCAICNHSQ--RTCAAS-----CGEFWD 41
Db 73 CPPHYTQFW-NYLERCYCNVLCGEREEARACHATHNACRACRTGFFAHAGFCLSHAS 131
Qy 42 LSPGDSVITPNACQSTLWPHSQAVERMAGDVQCGTSVPSTF-----LLWPH--- 90
Db 132 CPPAGVIAPTPSQNT-----QCQPCPGTFSASSSSSEQCQPHNC 174
Qy 91 -CLLSVSNMPCSSLPVLTCTCS 112
Db 175 TALGLALNVPGSSHDTLCTST 197

RESULT 11
Q62327 MOUSE
ID Q62327 MOUSE PRELIMINARY; PRT; 459 AA.
AC Q62327;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tumour necrosis factor receptor 2 protein (fragment).
GN Name=Tnfrsf1b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Amino acid variation in the tumor necrosis factor receptor 2 is
RT linked to autoimmune diabetes in NOD mice.";
RL Genomics 0:0-0(0).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NOD;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
RT gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -; mRNA.
DR PIR; I48854; I48854.
DR HSSP; P19438; INCF.
DR MGI; MGI:1314883; Tnfrsf1b.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
DR GO; GO:0019221; P:cytokine and chemokine mediated signaling p...; IEA.
DR InterPro; IPR011366; TNFRcpt_2.
DR InterPro; IPR011368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6_2.
DR PIRSF; PIRSF001968; TNFR_2; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00650; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 11.7%; Score 94; DB 2; Length 459;
Best Local Similarity 24.2%; Pred. No. 1.2;
Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;

Qy 16 TCMECKA-----ICNHQSORTCAASCGEFWDLSPGDSVITPNACQ-----STLWP 61
Db 78 TCLSCSSCSSTQDVETRACTKQQRVCAAGRYCALKTHS-----GSCRQCMRLSKGP 132
Qy 62 HSQVAERBMAGDVQCGTSVPSTF-----LLWPHCLLSVSNMPCSSLPVLTCTCSR 113

```

## RESULT 12

## TNFR1B\_MOUSE

## ID TNFR1B\_MOUSE

## STANDARD; PRT; 474 AA.

## AC P25119; O88734; P97893;

## DT 01-MAY-1992 (Rel. 22, Created)

## DT 01-MAY-1992 (Rel. 22, Last sequence update)

## DT 10-MAY-2005 (Rel. 47, Last annotation update)

## DE Tumour necrosis factor receptor superfamily member 1B precursor (Tumor

## necrosis factor receptor 2) (TNF-R2) (Tumor necrosis factor receptor

## type II) (p75) (p80 TNF-alpha receptor)."

## GN Name=Tnfrsf1b; Synonyms=Tnfr-2, Tnfr2;

## OS Mus musculus (Mouse).

## OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

## OC Muridae; Murinae; Mus.

## OX NCBI\_TaxID=10090;

## RN [1]

## RP NUCLEOTIDE SEQUENCE.

## RC MEDLINE=9118785; PubMed=1849278;

## RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H.,

## Chen E.Y., Goeddel D.V.;

## RT "Cloning and expression of cDNAs for two distinct murine tumor

## necrosis factor receptors demonstrate one receptor is species

## specific.";

## RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

## RN [2]

## RP NUCLEOTIDE SEQUENCE.

## RC MEDLINE=91246168; PubMed=1645445;

## RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,

## Copeland N.G., Jenkins N.A., Smith C.A.;

## RT "Molecular cloning and expression of the type 1 and type 2 murine

## receptors for tumor necrosis factor.";

## RL Mol. Cell. Biol. 11:3020-3026(1991).

## RN [3]

## RP NUCLEOTIDE SEQUENCE.

## RC MEDLINE=98414512; PubMed=9740674; DOI=10.1006/geno.1998.5407;

## RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;

## RT "The mouse tumor necrosis factor receptor 2 gene: genomic structure

## and characterization of the two transcripts.";

## RL Genomics 52:79-98(1998).

## RN [4]

## RP NUCLEOTIDE SEQUENCE OF 1-26.

## RC STRAIN=NOD;

## RA Jacob C.O., Liu J.;

## RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

## RN [5]

## RP NUCLEOTIDE SEQUENCE OF 1-22.

## RC TISSUE=Liver;

## RA Kissnerghis M., Fellows R., Feldmann M., Chernajovsky Y.;

## RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

## CC -1- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and

## approximately 5-fold lower affinity for homotrimeric

## TNFSF1/lymphotoxin-alpha. The TRAF1/TRAFA2 complex recruits the

## apoptotic suppressors BIRC2 and BIRC3 to TNFSF1B/TNFR2 (By

## similarity).

## CC -1- SUBUNIT: Binds to TRAF2 (By similarity).

## CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

## CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.

## CC -----

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## removed.

## CC -----

## CC

|                       |   |   |                |   |
|-----------------------|---|---|----------------|---|
| DR                    | EMBL; M60469;   | AAA39752.1;                                       | -;             | mRNA.   |
| DR                    | EMBL; M59378;   | AAA40463.1;                                       | -;             | mRNA.   |
| DR                    | EMBL; Y14619;   | CAA74969.1;                                       | -;             | Genomic_DNA.  |
| DR                    | EMBL; Y14620;   | CAA74969.1;                                       | JOINED;        | Genomic_DNA.  |
| DR                    | EMBL; Y14621;   | CAA74969.1;                                       | JOINED;        | Genomic_DNA.  |
| DR                    | EMBL; Y14622;   | CAA74969.1;                                       | JOINED;        | Genomic_DNA.  |
| DR                    | EMBL; Y14623;   | CAA74969.1;                                       | JOINED;        | Genomic_DNA.  |
| DR                    | EMBL; U39488;   | CAA85021.1;                                       | -;             | Genomic_DNA.  |
| DR                    | EMBL; X87128;   | AAA60618.1;                                       | -;             | Genomic_DNA.  |
| DR                    | PIR; B38634;  | B38634.   |                |   |
| DR                    | HSSP; P19438;   | INCF.   |                |   |
| DR                    | Ensembl; ENSMUSG0000028599;                                       | Mus musculus.                                     |                |   |
| DR                    | MGI; MGI1314883;  | Tnfrsf1b.   |                |   |
| DR                    | GO; GO:0005615;   | C:extracellular space;                            | TAS.           |   |
| DR                    | GO; GO:0016021;   | C:integral to membrane;                           | TAS.           |   |
| DR                    | GO; GO:0008219;   | P:cell death;                                     | IMP.           |   |
| DR                    | GO; GO:0008283;   | P:cell proliferation;                             | TAS.           |   |
| DR                    | GO; GO:0007166;   | P:cell surface receptor linked signal transdu. .; | IMP.           |   |
| DR                    | GO; GO:0006954;   | P:inflammatory response;                          | IMP.           |   |
| DR                    | InterPro; IPR001368;  | TNFR_C6.  |                |   |
| DR                    | InterPro; IPR011366;  | TNFRccept_2.                                      |                |   |
| DR                    | Pfam; PF00020;  | TNFR_C6; 2.                                       |                |   |
| DR                    | PIRSFP; PIRSFP01968;  | TNFR_2; 1.  |                |   |
| DR                    | SMART; SMO0208;   | TNFR; 4.  |                |   |
| DR                    | PROSITE; PS00652;   | TNFR_NGFR_1; 2.                                   |                |   |
| DR                    | PROSITE; PSS0050;   | TNFR_NGFR_2; 3.                                   |                |   |
| KW                    | Glycoprotein; Receptor; Repeat; Signal; Transmembrane.            |   |                |   |
| KF                    | SIGNAL  | 1 22  |                |   |
| FT                    | CHAIN   | 23 474  |                |   |
| FT                    | TOPO_DOM  | 23 258  |                | Tumor necrosis factor receptor superfamily member 1B. |
| FT                    | TRANSEM   | 259 288   |                | Extracellular (Potential).                            |
| FT                    | TOPO_DOM  | 289 288   |                | Potential.  |
| FT                    | REPEAT  | 39 77   |                | Cytoplasmic (Potential).                              |
| FT                    | REPEAT  | 78 119  |                | TNFR-Cys 1.   |
| FT                    | REPEAT  | 120 164   |                | TNFR-Cys 2.   |
| FT                    | REPEAT  | 165 203   |                | TNFR-Cys 3.   |
| FT                    | CARBOHYD  | 69 69   |                | TNFR-Cys 4.   |
| FT                    | CARBOHYD  | 195 195   |                | N-linked (GlcNAc. .) (Potential).                     |
| FT                    | DISULFID  | 40 54   |                | By similarity.  |
| FT                    | DISULFID  | 55 68   |                | By similarity.  |
| FT                    | DISULFID  | 58 76   |                | By similarity.  |
| FT                    | DISULFID  | 79 94   |                | By similarity.  |
| FT                    | DISULFID  | 97 111  |                | By similarity.  |
| FT                    | DISULFID  | 101 119   |                | By similarity.  |
| FT                    | DISULFID  | 121 127   |                | By similarity.  |
| FT                    | DISULFID  | 136 145   |                | By similarity.  |
| FT                    | DISULFID  | 139 163   |                | By similarity.  |
| FT                    | DISULFID  | 166 181   |                | By similarity.  |
| FT                    | CONFLICT  | 78 78   |                | D -> DSDTVCAD (in Ref. 3).                            |
| FT                    | CONFLICT  | 102 102   |                | T -> S (in Ref. 3).                                   |
| FT                    | CONFLICT  | 108 108   |                | I -> T (in Ref. 3).                                   |
| FT                    | CONFLICT  | 283 283   |                | I -> F (in Ref. 3).                                   |
| FT                    | CONFLICT  | 331 331   |                | S -> SS (in Ref. 3).                                  |
| FT                    | CONFLICT  | 360 360   |                | F -> S (in Ref. 3).                                   |
| FT                    | CONFLICT  | 436 436   |                | C -> Y (in Ref. 3).                                   |
| SEQ                   | SEQUENCE  | 474 AA; 50320 MW; 462EAE398C4D6563 CRC64;         |                |   |
| <hr/>                 |   |   |                |   |
| Query Match           |   | 11.7%;  | Score 94;      | DB 1; Length 474;                                     |
| Best Local Similarity |   | 24.2%;  | Pred. No. 1.3; |   |
| Matches 36;           |   | Conservative 17;                                  | Mismatches 64; | Indels 32; Gaps 6                                     |
| QY                    | 16 TCMPCKA-----ICNHQSORTCAASCGEFWLSPGDGVITPNACQPQ----             | STLWP 61  |                |   |
| Db                    | 93 TCLSCSSSCTTDQVEIRACTKQNRCVACEAGRYCALKNTHS-----GSCRQMRLSKGP 147 |   |                |   |
| QY                    | 62 HSQVAERPMAGDVQCGETSYPTF-----LLWPHCLLSVNPPCSLPRVLCTCSR 113      |   |                |   |
| Db                    | 148 GFGVASSRAPNGNVLCAPAGTFSDTTSZDVCRRPHRICSLAIPGNASTDAVCAPESP 207 |   |                |   |
| QY                    | 114 CLECMLSIIIFPOLP-PTQLSGL-----GFN 137                           |   |                |   |

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 Wilming L.G., Wyshaw-Borja A., Yanagisawa M., Yang I., Yang L.,  
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 Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
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 Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 Birney E., Hayashizaki Y.,  
 "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 Nature 420:563-573(2002).  
 [4]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;  
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 "Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes";  
 Genome Res. 10:1617-1630(2000).  
 [5]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 Konno H., Akiyama J., Nishi K., Kitsuani T., Tashiro H., Itoh M.,  
 Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,  
 "RIKEN integrated sequence analysis (RISA) system-384-format  
 sequencing pipeline with 384 multicapillary sequencer";  
 Genome Res. 10:1757-1771(2000).  
 [6]  
 NUCLEOTIDE SEQUENCE.  
 STRAIN=C57BL/6J; TISSUE=Liver, and Lung;  
 Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
 Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
 Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 Muramatsu M., Hayashizaki Y.,  
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL; AK004844; BAB23610.1; -; mRNA.  
 EMBL; AK004752; BAB23533.1; -; mRNA.  
 MGI; MGI:1314883; Thirflb.  
 DR GO: GO:0005615; C:extracellular space; TAS.  
 DR GO: GO:0016021; C:integral to membrane; TAS.  
 DR GO: GO:0008219; P:cell death; IMP.  
 DR GO: GO:0008283; P:cell proliferation; TAS.  
 DR GO: GO:0007166; P:cell surface receptor linked signal transdu. .; IMP.  
 DR GO: GO:0006954; P:inflammatory response; IMP.  
 KW Receptor.  
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 11.7%; Score 94; DB 2; Length 474;  
 Best Local Similarity 24.2%; Pred. No. 1.3;  
 Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;  
 16 TCMFCKA-----ICNHQSORTCAASGCEFWDLSPGDSVITPNACPO-----STLWP 61  
 93 TCLSCSSSTTDQVEIRACTQKQNRVCACGRVCAKTHS-----GSCQKRLSKGP 147  
 62 HSQVAERMAAGDVQCSTSPSTF-----LWPHCLLSVSNMPCSSPRVLTCCSR 113  
 148 GFGVASSRAPNGVNLKACAPGTFSDTTSSTDVCRPHRISILAIPGNASTDAVCAPEP 207

114 CLSCMLSIIFPQLP-PTQLSGL----GPN 137  
 208 TLSAIPRTLVSQPEPTRSQPLDQEPGPS 236  
 RESULT 14  
 Q700K0 RAT PRELIMINARY; PRT; 5141 AA.  
 AC Q700K0 RAT PRELIMINARY; PRT; 5141 AA.  
 DT 03-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE SCO-spondin.  
 GN Names=SCO-spondin;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Meinzel O.;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 EMBL; AJ629845; CAF33425.1; -; mRNA.  
 DR HSP; P01130; IAJJ.  
 DR GO: GO:0007155; P:cell adhesion; IEA.  
 DR InterPro; IPR006207; Cys\_knot\_C.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR011489; EMI.  
 DR InterPro; IPR000421; FAS8\_C.  
 DR InterPro; IPR001545; Gly\_hormoneB.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR002919; Prot\_inh\_CR\_TIL.  
 DR InterPro; IPR000884; TSP1.  
 DR InterPro; IPR006552; VWC\_out.  
 DR InterPro; IPR001007; VWF\_C.  
 DR InterPro; IPR001846; VWF\_D.  
 DR Pfam; PF07546; EMI; 1.  
 DR Pfam; PF00754; F5\_F8\_type\_C; 1.  
 DR Pfam; PF00057; Ldl\_recept\_a; 10.  
 DR Pfam; PF01826; TIL; 12.  
 DR Pfam; PF00090; TSP\_1; 24.  
 DR Pfam; PF00093; VWC; 1.  
 DR Pfam; PF00094; VWD; 3.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 DR SMART; SM00192; Ldla; 10.  
 DR SMART; SM00209; TSP1; 25.  
 DR SMART; SM00214; VWC; 5.  
 DR SMART; SM00215; VWC\_out; 9.  
 DR SMART; SM00216; VWD; 3.  
 DR PROSITE; PS01235; CTCK\_2; 1.  
 DR PROSITE; PS01186; EGF\_3; 1.  
 DR PROSITE; PS00022; FAS8C\_3; 1.  
 DR PROSITE; PS00261; GLYCO\_HORMONE\_BETA\_1; UNKNOWN\_2.  
 DR PROSITE; PS01209; LDLRA\_1; 8.  
 DR PROSITE; PS00068; LDLRA\_2; 10.  
 DR PROSITE; PS00092; TSP1\_24.  
 DR PROSITE; PS01208; VWF\_C\_1; UNKNOWN\_1.  
 DR PROSITE; PS0184; VWF\_C\_2; 2.  
 SQ SEQUENCE 5141 AA; 550644 MW; 1772AB67F02CASE3 CRC64;

Query Match 11.6%; Score 93; DB 2; Length 5141;  
 Best Local Similarity 26.0%; Pred. No. 18;  
 Matches 40; Conservative 11; Mismatches 43; Indels 60; Gaps 11;  
 4 CPBEQWYAALLGTC-MFCKAICNHQSORT-----CAASGCEFWDLSPGDSV-----IT 50  
 4814 CPFGQ----VLSCATLCPSFCSHLWEGTICVREPCQLGCG-----CPGQLLHSGTCIP 4864  
 51 PNAQPOSTL---W-----PHSQVAERMAAGDVQCSTSPSTFLLW---PHCLLSVSNMPCS 101  
 4865 PEACPCTRLSPGLTLPLEQAQELPSG-----TVLTWNCTHCTCQGGVFTCS 4913

QY 102 SLPRVLCTCSRCLCMLSIIFPOLPPTQLSGLG 135  
Db 4914 H-----TDCQEC-----PGEILQLG 4929

## RESULT 15

Q8AXCO XENLA  
ID Q8AXCO XENLA PRELIMINARY; PRT; 286 AA.  
AC Q8AXCO;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Riddle 4.  
GN Name=Rdd4;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Wardle F.C.; Sive H.L.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF465788; AA015689.1; -; mRNA.  
DR HSSP; P56682; ICCV.  
DR InterPro; IPR002919; Prot\_Inh\_CR\_TIL.  
DR Pfam; PF01826; TIL; 4.  
SQ SEQUENCE 286 AA; 31037 MW; 9C2DAB2E975DCE73 CRC64;

Query Match 11.2%; Score 90; DB 2; Length 286;  
Best Local Similarity 25.6%; Pred. No. 1.8;  
Matches 40; Conservative 13; Mismatches 59; Indels 44; Gaps 9;

QY 4 CPPEQYWAALLGTC-WECK-----AICNHQSORTCAASCGEFWDLSPGDS--VITPNAC 54  
Db 29 CAPNQVWNSCGTACPLNCQFNRPDPVCILSCQRC--FCKEPIYFQNGDSGPCVLPSC 86  
QY 55 POSTLWPHSQVAERWAGGV--CCGTSYPSSTELLWPHCLLSVNMPCSLPRVLCTCCS 112  
Db 87 PPSQV-----ESCAPNQVWNSCGTA-----CPLNCQNF--RNPPDVCILSCQ 126  
QY 113 RCLCMLSIIF-----POLPPTQLSGLGPN 137  
Db 127 RGCFCKEPIYFQNGTSGPCVLPSCPPSQVESCAPN 162

Search completed: December 20, 2005, 10:42:47  
Job time : 231 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 20, 2005, 10:33:34 ; Search time 38 seconds  
(without alignments)  
359.547 Million cell updates/sec

Title: US-10-618-797-2  
Perfect score: 803  
Sequence: 1 MRSCPEEQYWAALLGTCMFC.....FPQLPPTQLSLGPNIGGLL 142

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 98    | 12.2        | 1299   | 2 T43251 | furin (EC 3.4.21.7) |
| 2          | 94    | 11.7        | 459    | 2 I48854 | gene murine tumour  |
| 3          | 94    | 11.7        | 474    | 2 B38634 | tumor necrosis fac  |
| 4          | 85    | 10.6        | 589    | 2 C38128 | epithelin/granulin  |
| 5          | 84.5  | 10.5        | 1680   | 2 A43434 | furin (EC 3.4.21.7) |
| 6          | 83.5  | 10.4        | 1548   | 2 S34583 | serine proteinase   |
| 7          | 81    | 10.1        | 250    | 1 A49053 | CD27 antigen precu  |
| 8          | 80.5  | 10.0        | 593    | 1 GYHU   | granulin precursor  |
| 9          | 80    | 10.0        | 349    | 2 T43457 | hypothetical prote  |
| 10         | 79.5  | 9.9         | 1700   | 2 S08167 | Balbani ring 3 pr   |
| 11         | 78.5  | 9.8         | 1373   | 2 JE0095 | gastric mucin MUC5  |
| 12         | 77.5  | 9.7         | 2219   | 2 T27684 | hypothetical prote  |
| 13         | 77    | 9.6         | 981    | 2 S51604 | receptor-like tyro  |
| 14         | 77    | 9.6         | 1005   | 2 S49015 | receptor tyrosine   |
| 15         | 76.5  | 9.5         | 355    | 2 B64445 | polyferredoxin 4x2  |
| 16         | 76.5  | 9.5         | 589    | 2 B38128 | epithelin/granulin  |
| 17         | 75.5  | 9.4         | 732    | 1 MNXRW4 | nonstructural prot  |
| 18         | 74.5  | 9.3         | 591    | 2 I48141 | acroganin - guine   |
| 19         | 74.5  | 9.3         | 5376   | 2 T42215 | zonalhesin - mouse  |
| 20         | 73.5  | 9.2         | 810    | 2 T10756 | Nel-homolog protei  |
| 21         | 73.5  | 9.2         | 1737   | 2 T00209 | MEGF8 protein - hu  |
| 22         | 73.5  | 9.2         | 2871   | 2 A55624 | fibrillin-1 precu   |
| 23         | 73    | 9.1         | 230    | 2 A38346 | ultra-high-sulfur   |
| 24         | 73    | 9.1         | 260    | 1 A46517 | CD27 antigen precu  |
| 25         | 73    | 9.1         | 337    | 2 I47079 | folliculin - shee   |
| 26         | 73    | 9.1         | 344    | 2 I45894 | folliculin - bovi   |
| 27         | 73    | 9.1         | 991    | 2 I78843 | receptor protein-t  |
| 28         | 72.5  | 9.0         | 265    | 2 T33695 | hypothetical prote  |
| 29         | 72    | 9.0         | 546    | 2 T46718 | probable farnesyl   |

|    |      |     |      |          |                    |
|----|------|-----|------|----------|--------------------|
| 30 | 72   | 9.0 | 1827 | 2 T34288 | hypothetical prote |
| 31 | 71.5 | 8.9 | 1115 | 2 T11614 | probable poly(A)-s |
| 32 | 71.5 | 8.9 | 2155 | 2 T30197 | alpha tectorin - m |
| 33 | 71   | 8.8 | 907  | 2 T27317 | hypothetical prote |
| 34 | 70.5 | 8.8 | 264  | 2 T47183 | hypothetical prote |
| 35 | 70.5 | 8.8 | 417  | 2 T25050 | hypothetical prote |
| 36 | 70.5 | 8.8 | 532  | 2 T04748 | hypothetical prote |
| 37 | 70.5 | 8.8 | 835  | 2 JP0076 | nel protein - chic |
| 38 | 70   | 8.7 | 223  | 2 B38346 | ultra-high-sulfur  |
| 39 | 70   | 8.7 | 1642 | 2 T19130 | hypothetical prote |
| 40 | 70   | 8.7 | 2195 | 2 T34264 | hypothetical prote |
| 41 | 70   | 8.7 | 2761 | 2 T21064 | hypothetical prote |
| 42 | 70   | 8.7 | 3002 | 2 A47221 | fibrillin 1 precu  |
| 43 | 69.5 | 8.7 | 480  | 2 S52306 | zinc finger protei |
| 44 | 69.5 | 8.7 | 518  | 2 B86299 | hypothetical prote |
| 45 | 69.5 | 8.7 | 654  | 2 T30136 | hypothetical prote |

ALIGNMENTS

RESULT 1

T43251  
furin (EC 3.4.21.75) - fall armyworm  
N;Alternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serine  
C;Species: Spodoptera frugiperda (fall armyworm)  
C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 09-Jul-2004  
C;Accession: T43251  
R;Cieplik, M.; Klenk, H.  
submitted to the EMBL Data Library, January 1996  
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiperda  
A;Reference number: Z22368  
A;Accession: T43251  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-1299 <CIE>  
A;Cross-references: UNIPROT:Q26489; UNIPARC:UPI0000083055; EMBL:Z68888; NID:g1167859; PIR  
A;Experimental source: clone Sfurin 6; ovary  
C;Function:  
A;Description: responsible for the endoproteolytic processing of proproteins with specific  
C;Keywords: hydrolase; serine proteinase

|                       |       |                      |   |                                   |
|-----------------------|-------|----------------------|---|-----------------------------------|
| Query Match           | 12.2% | Score 98;            | DB 2;                                   | Length 1299;                      |
| Best Local Similarity | 25.9% | Pred. No. 0.44;      |   |                                   |
| Matches               | 36;   | Conservative         | 15;                                     | Mismatches 58; Indels 30; Gaps 7; |
| QY                    | 1     | MRSCPEEQYWAALLGTCMFC | KAICNHQSORT--CAASCGEFNDLSPGDSVITNACPQST | 58                                |
| Db                    | 781   | LQCCPDGYWEDSEASVCRP  | CAAHCAATCSEADGC-TSC                     | EHHLVLDHGTGCTMA---SCPPS- 835      |
| QY                    | 59    | LWPHSQVAERMA-----    | GGDVCGTSPSTFLLMPHCLLSV-----             | SNMP 99                           |
| Db                    | 836   | ---HYETEDDMCAKHESCD  | TGCGPGETQCVTCHPSTYALDGR                 | CVTSCTSPAYYADKKRKE 892            |
| QY                    | 100   | CSSLPRVLCTCCSR-CLEC  | 117                                     |                                   |
| Db                    | 893   | CMRCPVGCSTCTSAFCLSC  | 911                                     |                                   |

RESULT 2

I48854  
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I48854  
R;Powell, E.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.  
Mamm. Genome 5, 726-727, 1994  
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.  
A;Reference number: I48854; MUID:95178848; PMID:7873884  
A;Accession: I48854  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-459 <RES>

A;Cross-references: UNIPROT:Q62327; UNIPARC:UPI000000B7DE6; EMBL:X76401; NID:g433830; PID:  
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog  
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 11.7%; Score 94; DB 2; Length 459;  
Best Local Similarity 24.2%; Pred. No. 0.41;  
Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;

QY 16 TCWFKCA-----ICNHQSORTCAASCGRFWDLSFGDVSITFNACPO---STLWP 61

Db 78 TCUSSSSSCTDQVETRACTKQNRVCACEAGRYCALKTHS-----GSCRQCMRLSKCGP 132

QY 62 HSOVAERMAGDVGQCGTSPSTF-----LLWPHCLLSVSNMPCSSLPRVLCTCCSR 113

Db 133 GFGVASSRAPNGVNLKACAPGTFSDTSTDCRPHRICSIILAFGNASTDAVCAPEP 192

QY 114 CLECMLSIIPQLP-PTQLSGL-----GPN 137

Db 193 TLAIPRTLTVSQPEPTRSQPLDQEPGPS 221

# RESULT 3

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 09-Jul-2004

A;Accession: B38634; A40254; S54816

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: B38634

A;Molecule type: mRNA

A;Residues: 1-474 <LEW>

A;Cross-references: UNIPROT:P25119; UNIPARC:UPI0000003E93; GB:M60469; NID:g199827; PID:

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: A40254

A;Molecule type: mRNA

A;Residues: 1-474 <GOO>

A;Cross-references: UNIPARC:UPI0000003E93; GB:M60469; NID:g199827; PID:AAA39752.1; PID:

R;Kissooneghis, M.; Fallowes, R.; Feldmann, M.; Chernajovsky, Y.

submitted to the EMBL Data Library, May 1995

A;Description: Characterization of the promoter region of the murine p75-TNF receptor.

A;Reference number: S54816

A;Accession: S54816

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-22 <KIS>

A;Cross-references: UNIPARC:UPI000016CF95; EMBL:X87128; NID:g809043; PID:CAA60618.1; PID:

C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog

F;1-23/Domain: signal sequence #status predicted <SIG>

F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F;40-77/Domain: NGF receptor repeat homology <NG1>

F;79-120/Domain: NGF receptor repeat homology <NG2>

F;166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 11.7%; Score 94; DB 2; Length 474;

Best Local Similarity 24.2%; Pred. No. 0.42;

Matches 36; Conservative 17; Mismatches 64; Indels 32; Gaps 6;

QY 16 TCWFKCA-----ICNHQSORTCAASCGRFWDLSFGDVSITFNACPO---STLWP 61

Db 93 TCUSSSSSCTDQVETRACTKQNRVCACEAGRYCALKTHS-----GSCRQCMRLSKCGP 147

QY 62 HSOVAERMAGDVGQCGTSPSTF-----LLWPHCLLSVSNMPCSSLPRVLCTCCSR 113

Db 148 GFGVASSRAPNGVNLKACAPGTFSDTSTDCRPHRICSIILAFGNASTDAVCAPEP 207

QY 114 CLECMLSIIPQLP-PTQLSGL-----GPN 137

Db 208 TLAIPRTLTVSQPEPTRSQPLDQEPGPS 236

# RESULT 4

C38128

epithelin/granulin precursor - mouse

N;Alternate names: acrogranin; PC-cell-derived growth factor

C;Species: Mus musculus (house mouse)

C;Date: 10-Jul-1992 #sequence revision 10-Jul-1992 #text\_change 09-Jul-2004

C;Accession: C38128; S32503; I49468; A46705

R;Plowman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.

J. Biol. Chem. 267, 13073-13078, 1992

A;Title: The epithelin precursor encodes two proteins with opposing activities on epithel

A;Reference number: A38128; MUID:92317004; PMID:1618805

A;Accession: C38128

A;Molecule type: mRNA

A;Residues: 1-589 <PLO>

A;Cross-references: UNIPROT:P28798; UNIPARC:UPI0000142953; GB:X62321; NID:g50851; PIDN:C1

R;Baba, T.; Nemoto, H.; Watanabe, K.; Arai, Y.; Gerton, G.L.

FEBS Lett. 322, 89-94, 1993

A;Title: Exon/intron organization of the gene encoding the mouse epithelin/granulin precu

A;Reference number: S32503; MUID:93245391; PMID:8482392

A;Accession: S32503

A;Molecule type: DNA

A;Residues: 18-349, 'L', 351-589 <BAB>

A;Cross-references: UNIPARC:UPI0000177C83

R;Baba, T.; Hoff, H.B.

Mol. Reprod. Dev. 34, 233-243, 1993

A;Title: Acrogranin, an acrosomal cysteine-rich glycoprotein, is the precursor of the gro

A;Reference number: I48141; MUID:93228994; PMID:8471244

A;Accession: I49468

A;Status: preliminary; translated from GB/EMBL/DBEJ

A;Molecule type: mRNA

A;Residues: 1-250, 'L', 252-253, 'V', 255-349, 'L', 351-401, 'SA', 404-589 <RES>

A;Cross-references: UNIPARC:UPI000016CBE7; GB:M86736; NID:g191766; PIDN:AAA37191.1; PID:

R;Zhou, J.; Gao, G.; Crabb, J.W.; Serrero, G.

J. Biol. Chem. 268, 10863-10869, 1993

A;Title: Purification of an autocrine growth factor homologous with mouse epithelin precu

A;Reference number: A46705; MUID:93266526; PMID:8496151

A;Accession: A46705

A;Status: preliminary

A;Molecule type: protein

A;Residues: 18-19, 'X', 21-25, 'X', 27-29, 'XX', 32, 'XXX', 119-127, 152-154, 'DXK', 158-161, 'X', 16:

A;Cross-references: UNIPARC:UPI0000177C84; UNIPARC:UPI0000177C85; UNIPARC:UPI0000177C86;

C8B

C;Superfamily: granulin

Query Match 10.6%; Score 85; DB 2; Length 589;

Best Local Similarity 20.4%; Pred. No. 3.3;

Matches 48; Conservative 18; Mismatches 67; Indels 102; Gaps 13;

QY 3 SCPEEQYMAAL---LGTCWFCKAIC-----NHQSORTCA----- 33

Db 287 SCPEGYTCRLMTNGAWCCPFKAVACCEBHIHCCPAGFQCHTEKGTCEMGILQVPMKKV 346

QY 34 -----ASCGEF-----WDLSPGDSVI-----TPNACPQS- 57

Db 347 IAPRRLPDPQLKLSDFCDFTFTRCPNTNCTCKLNSGDWGCPIPEAVCCSDNQHCPCQGF 406

QY 58 --TLWPHSQVAERHAG-----GDVQCG--TSYPSTFLWPHCLLSV-SNM 98

Db 407 TCLAQGYCQKGDVTWAGLEKIPARQTPPLQIGDGDQHTSCB-----VGQTCFSLKGSW 462

QY 99 PCSLSPLVLC-----TCCSRCLCMLSIIFPQLPPTQLSGLGNIGGL 141

Db 463 ACCQLPHAVCCEDRQHCPCPAGYTCNVKARTCEKVDVFQ-PPVLLT-LGPKVGNV 515

# RESULT 5

A43434

furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster



C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A43434  
R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E.  
J. Biol. Chem. 267, 17208-17215, 1992  
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc  
A;Reference number: A43434; MUID:92381036; PMID:1512259  
A;Accession: A43434  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1680 <ROE>  
A;Cross-references: UNIPROT:P30432; UNIPARC:UPI000016BC03; GB:M94375; NID:9157461; PID:9  
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBI:P11934)  
C;Genetics:  
A;Gene: FlyBase:Fur2  
A;Cross-references: FlyBase:FBgn0004598  
C;Keywords: hydrolase; serine proteinase; transmembrane protein  
F;409-552/Domain: subtilisin homology <SBT>  
F;418-457,638/Active site: Asp, His, Ser #status predicted

Query Match 10.5%; Score 84.5; DB 2; Length 1680;  
Best Local Similarity 28.3%; Pred. No. 8.9;  
Matches 32; Conservative 14; Mismatches 40; Indels 27; Gaps 6;

Qy 4 CPEQYWAALLGTCMFCCKAICNHQSQRTCAASCGEFWDLSPGDSVITPNACPOSTLWPHS 63  
Db 1199 CSESEFYQVEGQC-----RPCHASGSC--NGPADTCT--SCPPNRLLEQS 1242  
Qy 64 QVAERWAGGVDQCTSYPTFLWPHCLLSVSNMPCSSLPVLCTCCSCLE 116  
Db 1243 RCVSGCGREGPFVEAGS-----LCSPCLHTCSQ--CVS--RTNCSNCSRGLE 1284

RESULT 6  
S34583  
serine proteinase (BC 3.4.21.-) PC6B - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S34583  
R;Nakagawa, T.; Murakami, K.; Nakayama, K.  
FEBS Lett. 327, 165-171, 1993  
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
A;Reference number: S34583; MUID:93327934; PMID:8335106  
A;Accession: S34583  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1548 <NAK>  
A;Cross-references: UNIPROT:Q04592; UNIPARC:UPI0000016CF9E; GB:D17583; NID:9407344; PIDM:  
C;Keywords: hydrolase; serine proteinase

Query Match 10.4%; Score 83.5; DB 2; Length 1548;  
Best Local Similarity 29.3%; Pred. No. 10;  
Matches 39; Conservative 5; Mismatches 52; Indels 37; Gaps 9;

Qy 3 SCPEQYWAALLGTCMFCCKAICNHQSQRTCAASCGEFWDLSPGDSVITPNACPOSTL 59  
Db 963 SCPEGFY--AKDGVCEHCSSPC-----KTCGNATSCNS---CEGDFVLHDGVC----- 1006  
Qy 60 W----PHSQVAERWAG-----GDVCGTSYPTFLWPHCLLSVSNMPCSSLP-- 104  
Db 1007 WKTCPKHKHVAEGVCKRCPQCQDIHKTCKECPDPFFLYNDMCHRS---CPKSFYPM 1063  
Qy 105 RVLCTCCSRLEC 117  
Db 1064 RQCVPHCNCLC 1076

RESULT 7  
A49053  
CD27 antigen precursor - mouse  
N;Alternate names: CD27L receptor; T cell activation antigen CD27  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Dec-1993 #sequence\_revision 22-Apr-1995 #text\_change 09-Jul-2004  
C;Accession: A49053

R;Graveststein, L.A.; Blom, B.; Nolten, L.A.; de Vries, E.; van der Horst, G.; Ossendorp, E.  
Eur. J. Immunol. 23, 943-950, 1993  
A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyte  
A;Reference number: A49053; MUID:93209296; PMID:8384562  
A;Accession: A49053  
A;Molecule type: mRNA  
A;Residues: 1-250 <GRA>  
A;Cross-references: UNIPROT:P41272; UNIPARC:UPI0000023489  
A;Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBI:P128169)  
C;Superfamily: CD27 antigen; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; homodimer; receptor; surface antigen; T-cell; tra  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-250/Product: CD27 antigen #status predicted <MAT>  
F;21-182/Domain: extracellular #status predicted <EXT>  
F;27-63/Domain: NGF receptor repeat homology <NG1>  
F;65-105/Domain: NGF receptor repeat homology <NG2>  
F;121-179/Region: proline/serine/threonine-rich  
F;193-202/Domain: transmembrane #status predicted <TMN>  
F;203-250/Domain: intracellular #status predicted <INT>  
F;95,162/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 81; DB 1; Length 250;  
Best Local Similarity 20.7%; Pred. No. 3.6;  
Matches 35; Conservative 12; Mismatches 46; Indels 76; Gaps 9;

Qy 9 YWAALLGTCMFCCKAICNHQSQRTCAASCGEFWDLSPGDSVITPNACPOSTLWPHSQA-- 66  
Db 7 YWLCMLGTLVGLSA-----TLAPNSCDPKHYWTGGGLCCR 41  
Qy 67 -----EERMAGGDVQC-----GTSYPTFLWPHCL-----LSVSNMPC 100  
Db 42 MCEPPTGTFVVKDCQDRTA---AQCPCIPGTSFDPVHTPHCESCRHNSGFLIRN--C 96  
Qy 101 SSLPRVLCTC-----C--SRCLEC-----MLSIIFPOLPPQL 131  
Db 97 TVTNAECSCKNWCQRCDECTEDPPLNPALTRQPSPTSPSPPPPHL 145

RESULT 8  
GYHU  
granulin precursor [validated] - human  
N;Alternate names: epithelin  
N;Contains: granulin A; granulin B; granulin C; granulin D; granulin E; granulin F; gran  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1992 #sequence\_revision 03-May-1996 #text\_change 31-Dec-2004  
C;Accession: JCI284; A38128; A38118; A36698; B36698; C36698; D36698; A56873  
R;Bhandari, V.; Bateman, A.  
Biochem. Biophys. Res. Commun. 188, 57-63, 1992  
A;Title: Structure and chromosomal location of the human granulin gene.  
A;Reference number: JCI284; MUID:93038704; PMID:1417868  
A;Accession: JCI284  
A;Molecule type: DNA  
A;Residues: 1-593 <SHA>  
A;Cross-references: UNIPROT:P28799; UNIPROT:Q9UCH0; UNIPARC:UPI00000015E0  
R;Floman, G.D.; Green, J.M.; Neubauer, M.G.; Buckley, S.D.; McDonald, V.L.; Todaro, G.J.  
J. Biol. Chem. 267, 13073-13078, 1992  
A;Title: The epithelin precursor encodes two proteins with opposing activities on epithel  
A;Reference number: A38128; MUID:92317004; PMID:1618805  
A;Accession: A38128  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-593 <PLO>  
A;Cross-references: UNIPARC:UPI00000015E0; GB:X62320; NID:931192; PIDN:CAA44196.1; PID:9  
R;Bhandari, V.; Palfree, R.G.E.; Bateman, A.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1715-1719, 1992  
A;Title: Isolation and sequence of the granulin precursor cDNA from human bone marrow rev  
A;Reference number: A38118; MUID:92179253; PMID:1542665  
A;Accession: A38118  
A;Molecule type: mRNA  
A;Residues: 1-406, 'R', 408-433 'G', 435-453 'G', 455-459 'Q', 461-546 'A', 548-566 'R', 568-59  
A;Cross-references: UNIPARC:UPI0000151BFF; GB:W75161; NID:9183612; PIDN:AA58617.1; PID:  
A;Note: this sequence has been revised in reference JCI284  
R;Bateman, A.; Belcourt, D.; Bennett, H.; Lazure, C.; Solomon, S.

Biochem. Biophys. Res. Commun. 173, 1161-1168, 1990

A>Title: Granulins, a novel class of peptide from leukocytes.

A|Reference number: A36698; MUID:91097544; PMID:2268320

A|Accession: A36698

A|Molecule type: protein

A|Residues: 281-336 <BAT>

A|Cross-references: UNIPARC:UPI00001744F2

A|Note: this protein was purified and characterized as granulin A

A|Accession: B36698

A|Molecule type: protein

A|Residues: 206-218, 'H', 220-233 <BA2>

A|Cross-references: UNIPARC:UPI00001744F3

A|Note: this protein was purified and characterized as granulin B

A|Accession: C36698

A|Molecule type: protein

A|Residues: 364-367, 'X', 369-385, 'H', 387-396 <BA3>

A|Cross-references: UNIPARC:UPI00001744F4

A|Note: this protein was purified and characterized as granulin C

A|Accession: D36698

A|Molecule type: protein

A|Residues: 442-446, 'XDTRSS', 456-458, 'DG' <BA4>

A|Cross-references: UNIPARC:UPI00001744F5

R|Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.  
Br. J. Cancer 67, 686-692, 1993

A>Title: Characterisation of UGP and its relationship with beta-2-microglobulin

A|Reference number: A56873; MUID:93229246; PMID:8471426

A|Accession: A56873

A|Molecule type: protein

A|Residues: 281-283, 'X', 285-289, 'S', 291-295 <KAR>

A|Cross-references: UNIPARC:UPI0000070B1b

A|Experimental source: urine

A|Note: sequence extracted from NCBI backbone (NCBIP:129524)

C|Genetics:

A|Gene: GDB:GRN

A|Cross-references: GDB:136006; OMIM:138945

A|Map position: 17pter-17qter

A|Introns: 46/3; 88/3; 117/1; 154/3; 200/1; 236/3; 279/1; 311/3; 312/1

C|Keywords: glycoprotein; tandem repeat

F|1-17/Domain: signal sequence #status predicted <SIG>

F|18-593/Product: granulin #status predicted <WAT>

F|18-593/Product: progranulin #status predicted <PRO>

F|18-44/Product: paraganulin #status experimental <PGR>

F|58-113/Product: granulin G #status predicted <GRG>

F|123-179/Product: granulin F #status predicted <GRF>

F|266-361/Product: granulin B #status experimental <GRB>

F|281-366/Product: granulin A #status experimental <GRA>

F|364-417/Product: granulin C #status experimental <GRC>

F|442-496/Product: granulin D #status predicted <GRD>

F|518-573/Product: granulin E #status predicted <GRE>

F|368/Binding site: carbohydrate (Asn) (covalent) #status experimental

|                       |        |   |       |  |     |        |      |
|-----------------------|--------|---|-------|--|-----|--------|------|
| Query Match           | 10.0%; | Score   | 80.5; | DB   | 1;  | Length | 593; |
| Best Local Similarity | 24.2%; | Pred. No.   | 8.4;  |  |     |        |      |
| Matches               | 31;    | Conservative  | 16;   | Mismatches   | 64; | Indels | 17;  |
|                       |        |   |       |  |     | Gaps   | 6;   |
| Qy                    | 3      | SCPEE   | ---   | QYWAALLGTCMFCAICNHQSORTCAASGGEFWDLSPGDSVITPNACPOST | 58  |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |
| Db                    | 289    | SCPQGYTCCLRQSGAWGCCPPTQVACEDHITHCCPA--GFTCDTQKGTCEGPHQVPMWE   | 346   |  |     |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |
| Qy                    | 59     | LWP-HSQVABERMAAGDVQCG--TSYSPSTFLLWPHCLLSVSNMPCSSLPRVLCT-----C | 110   |  |     |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |
| Db                    | 347    | KAPAHLSLPDQALKRDPVPCDNVSSCSDDFC---CQLTSGEWGCCPTPEAVCCSDHQHC   | 403   |  |     |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |
| Qy                    | 111    | CSRCLECM  | 118   |  |     |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |
| Db                    | 404    | CPOGYTCV  | 411   |  |     |        |      |
|                       |        | :   | :     | :  | :   | :      | :    |

RESULT 9  
T43457 hypothetical protein DKF2p434E2321.1 - human (fragment)  
C/Spectes: Homo sapiens (man)  
C/Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text

C;Accession: T43457  
R;Blum, H.; Bausachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence database, December 1999  
A;Reference number: Z22517  
A;Accession: T43457  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-349 <NA>  
A;Cross-references: UNIPROT:Q9UF43; UNIPARC:UPI0000072EF6; EMBL:AL133619  
A;Experimental source: adult testis; clone DKFZp434E23z1  
C;Genetics:  
A;Note: DKFZp434E23z1.1

|    | Query Match           | 10.08;  | Score 80;      | DB 2;          | Length 349;        |
|----|-----------------------|---|----------------|----------------|--------------------|
|    | Best Local Similarity | 25.96;  | Pred. No. 5.9; |                |                    |
|    | Matches 38;           | Conservative  | 13;            | Mismatches 46; | Indels 50; Gaps 9; |
| Qy | 10                    | WAALLGT-----CMFCKAIGN-----HQSORTCAASCGE-----                  | 39             |                |                    |
| Db | 70                    | WAATMTGKGSRVLPFCHLSKALPHDPDSGHPAQDSGLWSRAHPFLSLGLTSGGHLTG     | 129            |                |                    |
| Qy | 40                    | -WDLSPGDSVITPNACPOSTLMPHQSVAERMAAGDV--QCQTSYPSTFTLLMPHCLLSVS  | 96             |                |                    |
| Db | 130                   | GWS-QPGN--IVAGAVPRAL--PSQDWMENGVEGGPPFPRCGN---SSSELFMAKCGPSRQ | 181            |                |                    |
| Qy | 97                    | NMPCSS-----LPRVLCTCCSRC                                       | 114            |                |                    |
| Db | 182                   | POPCAGDADRTRTEAMLSLGTCCSMC                                    | 208            |                |                    |

**RESULT 10**

S08167

Balbiani ring 3 protein - midge (Chironomus tentans)

C;Species: Chironomus tentans

C:\Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 16-Aug-2004

C;Accession: S08167

R;Paulsson, G.; Lendahl, U.; Gal

J. Mol. Biol. 211, 331-349, 1990

A;Title: The balbiani ring 3 gene in *Chironomus tentans*

A;Reference number: S08167; MUID:90172404; PMID:16

A;Accession: S08167

A; Status: not compared with  
A-Melocula time. DNA

A; Molecule type: DNA  
A: Position: 1-1700 / 1811

A; Kevlars  
A: Cross-ref

A; Cross-Rel  
C-Genetics

A: Gene: BR3

A: Map position: 4

| Query Match | 9.9% | Score 79.5 | DB 2 | Length 1700 |
|-------------|------|------------|------|-------------|
|-------------|------|------------|------|-------------|

Best Local Similarity 26.0%; Pred. No. 25;

|         |     |              |     |            |     |        |     |      |     |
|---------|-----|--------------|-----|------------|-----|--------|-----|------|-----|
| Matches | 39; | Conservative | 15; | Mismatches | 47; | Indels | 49; | Gaps | 11; |
|---------|-----|--------------|-----|------------|-----|--------|-----|------|-----|

13

QY 3 SCP-EEQYWAALLGTCMFCKAIC-NHQSQRTCAASCGEFFWDLSPGD-SVIT----- 50

Db 818 ACPNKKQCKAPLWVSDEFCDVCPCNSAMKTC-----LSPKEWNKVTTCTCDCNPPK 868

QY 51 PNACQSTLWPHSQV-----AEERMAG-----DVQCGTSYPSTFL-----LWP-----H 90

[illegible]

db 869 PDCCPGTQKWMDDKCKCKGCPNAQTDCAGGKKFNDFTCSCGCPSGKLDCTGNTKWSAETCT 928

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QY 91 CLLSVSNMPCSSLPRV---LCTCCSRCTEC 117

250  
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DB 929 CGCGDVNRNCGNLGNFNFDNLCC-----EC 953

**SECRET**

## RESULTS

JE0095  
active mucin MIC50 - human

gASTRIC MUCIN MUC5AC PRECURSOR - human  
C.SPECIES: Homo sapiens (man)

```
C:\species: HOMIO saprems (man)
C:\Date: 22-May-1998 #sequence revision 29-May-1998 #text change 09-Jul-2004
```

C>Date: 22-May-1998 #sequence\_revision 23 may 1998 #contam\_exchange 23 may 1998  
C:Accession: JE0095

```
C:\species: Homo sapiens (man)
C:\Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text change 09-Jul-2004
```

Biochem. Biophys. Res. Commun. 245, 853-859, 1998  
A;Title: Molecular cloning of human gastric mucin MUC5AC reveals conserved cysteine-rich  
A;Reference number: JE0095; MUID:98249803; PMID:9588204

A;Accession: JE0095  
A;Molecule type: mRNA  
A;Residues: 1-1373 <BOV>  
A;Cross-references: UNIPROT:O75372; UNIPARC:UPI000017C12D; GB:AF043909  
A;Experimental source: stomach  
E;1-19/Domain: signal sequence #status predicted <SIG>  
F;273-300/Domain: leucine zipper #status predicted <LZP>

Query Match 9.8%; Score 78.5; DB 2; Length 1373;  
Best Local Similarity 22.8%; Pred. No. 26;  
Matches 39; Conservative 14; Mismatches 53; Indels 65; Gaps 11;  
Qy 8 QYWAALL-----GT-----CMFKCAINHQSQRTCAA-----SCGE--- 38  
Db 630 QHWCQLTDADGPFGRCHAAVKPGTYTYSNCFDTCNCRSEDCLCAALLSYVHACAAGV 689  
Qy 39 ---FMDLSPGDSVITP--NACQSTLPHSQVAE-----ERMAGDVQCGTSY----- 81  
Db 690 QLGNW----RDGVCTKPMWTCPKSMY-HYHVSTCQPTCRSLSGDITCSVGFIPVDGCI 744  
Qy 82 --PSTFLWPHCLLSVNMPC-----SSLPR-----VLCTCCSRCLCQM 118  
Db 745 CPKGTFLDDTKCKVQASNCPCYHRGSMIPNGESVHDSGAICTCTHGLSCI 795

## RESULT 12

T27684  
hypothetical protein ZK1067.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
A;Accession: T27684  
R;Thomas, K.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: Z20404  
A;Accession: T27684  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-2219 <WIL>  
A;Cross-references: UNIPROT:Q23388; UNIPARC:UPI00000761CD; EMBL:Z70038; PIDN:CAA93884.1  
A;Experimental source: clone ZK1067  
C;Genetics:  
A;Gene: CESP:ZK1067.2  
A;Map position: 2  
A;Introns: 139/3; 246/3; 487/3; 784/1; 960/2; 1067/3; 1113/3; 1171/3; 1321/2; 1383/3; 14

Query Match 9.7%; Score 77.5; DB 2; Length 2219;  
Best Local Similarity 20.9%; Pred. No. 48;  
Matches 31; Conservative 16; Mismatches 44; Indels 57; Gaps 7;  
Qy 2 RSCPEQYWAALLGTCMF-----CGSLYVEVTLDCGHRITTPCSRINSKCDQSCPKLLCGH---C--KAICNHQSQRTC 32  
Db 1577 KACVEE-----CGSLYVEVTLDCGHRITTPCSRINSKCDQSCPKLLCGH---AC 1626  
Qy 33 AASCGEFDLSPGDSVIT--PNACQSTLPHSQVAERMAGDVQCGTSYPSTFLWPH 90  
Db 1627 AAKCGEFTLVSECSQLVGMPFLSCGHIKQLTCSKISANEI---DLTCDQCEKTMACPH 1683  
Qy 91 CLLSVSNMPCSSLPVLCTCCSRCLCQM 118  
Db 1684 KCABICQPCPT-----VECM 1698

## RESULT 13

S51604  
receptor-like tyrosine kinase Etk-1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 29-May-1998  
A;Accession: S51604  
R;Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993

A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A;Reference number: S49015; MUID:94067777; PMID:7504232  
A;Accession: S51604  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-981 <MAI>  
A;Cross-references: UNIPARC:UPI0000175666; EMBL:S68029  
A;Note: the authors translated the codon GAC for residue 170 as Glu  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
E;1-19/Domain: protein kinase homology <KIN>  
F;651-917/Domain: protein kinase homology <KIN>  
F;659-667/Region: protein kinase ATP-binding motif

Query Match 9.6%; Score 77; DB 2; Length 981;  
Best Local Similarity 26.5%; Pred. No. 26;  
Matches 36; Conservative 7; Mismatches 61; Indels 32; Gaps 8;  
Qy 4 CPBEQYWAALLGTCMFCKAICNHQSQRTCAASCGEFDLSPGDSVITPNACQSTLWPHS 63  
Db 278 CSAEGEWLVPIGKCM-CKA-GYEKNGTCQVCRPGFKASPHSQ--TCSKCP-----PHS 328  
Qy 64 QVAERWAGDVQCGTSY-----PSTFLWPHCLLSVSNMPCSSLPVLCTCCSRCLC 117  
Db 329 YTHEE--ASTSCVCEKDYFRRESDPPT-----MACTRPPSAPRNAISVNYE- 372  
Qy 118 MLSIIFPQPTQLSG 133  
Db 373 -TSVFLEWIPPADTGG 387

## RESULT 14

S49015  
receptor tyrosine kinase Etk-1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
A;Accession: S49015; S51602  
R;Maisonnier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam  
A;Reference number: S49015; MUID:94067777; PMID:7504232  
A;Accession: S49015  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1005 <MAI>  
A;Cross-references: UNIPROT:P54757; UNIPARC:UPI0000050E88; EMBL:S68024  
A;Note: the authors translated the codon GAC for residue 170 as Glu  
A;Accession: S51602  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-305, 'G', 359-1005 <MA2>  
A;Cross-references: UNIPARC:UPI0000175665; EMBL:S68026  
A;Note: the authors translated the codon GAC for residue 170 as Glu  
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
E;675-941/Domain: protein kinase homology <KIN>  
F;683-691/Region: protein kinase ATP-binding motif

Query Match 9.6%; Score 77; DB 2; Length 1005;  
Best Local Similarity 26.5%; Pred. No. 27;  
Matches 36; Conservative 7; Mismatches 61; Indels 32; Gaps 8;  
Qy 4 CPBEQYWAALLGTCMFCKAICNHQSQRTCAASCGEFDLSPGDSVITPNACQSTLWPHS 63  
Db 278 CSAEGEWLVPIGKCM-CKA-GYEKNGTCQVCRPGFKASPHSQ--TCSKCP-----PHS 328  
Qy 64 QVAERWAGDVQCGTSY-----PSTFLWPHCLLSVSNMPCSSLPVLCTCCSRCLC 117  
Db 329 YTHEE--ASTSCVCEKDYFRRESDPPT-----MACTRPPSAPRNAISVNYE- 372  
Qy 118 MLSIIFPQPTQLSG 133  
Db 373 -TSVFLEWIPPADTGG 387

## RESULT 15

E64445  
polyferredoxin 4x2[4Fe-4S] fwdF - Methanococcus jannaschii  
N/Alternate names: formylmethanofuran dehydrogenase (tungsten) chain F [misnomer]  
C/Species: Methanococcus jannaschii  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 05-Oct-2004  
C/Accession: E64445  
R/Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Overbeek, R.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; rsion, J.D.; Sadow, P.W.; 1058-1073, 1996  
Science 273, 1058-1073, 1996  
A/Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A/Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A/Reference number: A64300; MUID:96337999; PMID:8688087  
A/Accession: E64445  
A/Status: nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-355 <BUL>  
A/Cross-references: UNIPROT:Q58566; UNIPARC:UPI0000066ADC; GB:U67558; GB:L77117; NID:gl5  
C/Genetics:  
A/Map position: FOR1106732-1107799  
C/Suprafamily: formylmethanofuran dehydrogenase, subunit F;ferredoxin 2[4Fe-4S] homolog  
C/Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein  
F/109-174/Domain:ferredoxin 2[4Fe-4S] homology <FER3>  
F/33,36,39,83/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/43,73,76,79/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/117,120,123,166/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/127,156,159,162/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/136,139,202,254/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/206,244,247,250/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/276,279,282,323/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted  
F/286,313,316,319/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 9.5% Score 76.5; DB 2; Length 355;  
Best Local Similarity 20.8%; Pred. No. 12;  
Matches 30; Conservative 20; Mismatches 45; Indels 49; Gaps 8;  
Qy 17 CMFCKA---ICNHQSORTCAASC-----GEFWDLSPGDSVITPNAFCQ----STLWP 61  
Db 196 CVFCKVCFVCPHDAIEVICYKCPMKRIPQAKLIYEDITGKTVIDKACVTCGWCAFCIP 255  
Qy 62 HSQVAERMAAGDV-----QCGTSTPSTFLLWPHCLLSVSNMPCSL-----P 104  
Db 256 AEAIEVEKPFKGLIIDVNAACNA-----CGACISICPCSALEFPKPKDKAEKVP 304  
Qy 105 RV-----LCTCCSRCLR-CMLSII 122  
Db 305 RIIVNQNLVLCGACAKACPVNAI 328

Search completed: December 20, 2005, 10:43:31

Job time : 41 secs